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OM protein - protein search, using sw model

Run on: July 27, 2004, 17:26:21 ; Search time 20 Seconds
(without alignments)
1701.076 Million cell updates/sec

Title: US-09-802-285A-2

Perfect score: 3494

Sequence: 1 MTTKIFRIIVFAVIALSSG.....KGKLNLTITNGKQOLVLP 659

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/6C COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3494	100.0	659	1	US-08-258-639A-4
2	3494	100.0	659	2	US-08-900-951-4
3	3494	100.0	659	5	PCT-US95-07391A-4
4	164	4.7	649	4	US-09-134-000C-5302
5	126.5	3.6	698	4	US-09-134-001C-3632
6	124	3.5	23	1	US-08-258-639A-9
7	124	3.5	23	5	PCT-US95-07391A-9
8	124	3.5	23	5	US-08-900-951-9
9	119	3.4	23	1	US-08-258-639A-10
10	119	3.4	23	2	US-08-900-951-10
11	119	3.4	23	5	PCT-US95-07391A-10
12	119	3.4	1138	1	US-07-973-320-2
13	119	3.4	1138	1	US-07-973-320-4
14	118	3.4	772	1	US-08-258-639A-2
15	118	3.4	772	2	US-08-900-951-2
16	118	3.4	772	5	PCT-US95-07391A-2
17	117.5	3.4	1028	4	US-09-543-681A-7181
18	116	3.3	4536	4	US-09-180-422B-27
19	116	3.3	4536	4	US-09-079-030-1
20	115.5	3.3	1168	1	US-08-620-717A-9
21	114.5	3.3	1167	1	US-08-485-568A-6
22	114.5	3.3	1167	2	US-08-590-554A-6
23	114.5	3.3	1167	2	US-09-184-223-6
24	113.5	3.2	1398	1	US-08-750-532-9
25	113.5	3.2	1398	3	US-08-894-818B-8
26	113.5	3.2	1398	4	US-09-445-472-6
27	111	3.2	927	4	US-09-134-001C-4831

28 110 3.1 4563 4 US-09-108-006C-1 Sequence 1, Appli
29 109 3.1 951 3 US-08-816-346-58 Sequence 58, Appli
30 109 3.1 951 3 US-09-335-411-58 Sequence 58, Appli
31 109 3.1 952 2 US-08-788-674-5 Sequence 5, Appli
32 109 3.1 952 3 US-08-816-346-4 Sequence 4, Appli
33 109 3.1 952 3 US-09-335-411-4 Sequence 4, Appli
34 108.5 3.1 1096 4 US-09-134-000C-5764 Sequence 5764, Ap
35 108 3.1 1015 4 US-09-134-000C-6204 Sequence 6204, Ap
36 106 3.0 884 4 US-09-328-352-4598 Sequence 4598, Ap
37 106 3.0 945 4 US-09-198-452A-1030 Sequence 1030, Ap
38 106 3.0 1375 3 US-09-210-361-4 Sequence 4, Appli
39 106 3.0 1375 4 US-09-740-274-4 Sequence 4, Appli
40 105 3.0 443 4 US-09-328-352-6322 Sequence 6322, Ap
41 105 3.0 741 4 US-09-252-991A-22440 Sequence 22440, A
42 105 3.0 965 4 US-09-437-277-3 Sequence 3, Appli
43 104 3.0 1742 4 US-09-386-962C-4 Sequence 4, Appli
44 104 3.0 1849 4 US-08-851-567B-49 Sequence 49, Appli
45 104 3.0 2516 4 US-08-851-567B-47 Sequence 47, Appli

ALIGNMENTS

RESULT 1
US-08-258-639A-4
; Sequence 4, Application US/08258639A
; Patent No. 5681733
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
; APPLICANT: Blain, Francoise
; APPLICANT: Bennett, Clark
; APPLICANT: Gu, Kangfu
; APPLICANT: Zimmermann, Joseph
; APPLICANT: Musil, Roy
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/258,639A
; FILING DATE: 10 JUNE 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Healey, William J.
; REGISTRATION NUMBER: 36,160
; REFERENCE/DOCKET NUMBER: 104385.116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942-8400
; TELEFAX: (202)942-8484
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 659 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-258-639A-4
Query Match 100.0%; Score 3494; DB 1; Length 659;
Best Local Similarity 100.0%; Pred. No. 4.1e-308;
Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTTKIFRIIVFAVIALSSGILQSSSITKDFHINLEYSGLKYNKVAAGNYDDAA 60

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Db 1 MTTKIFKRIIVFAVIALSSGNILAQSSITRKDFDHINLEYSGLKKNKAVAAAGNYDDAA 60
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Db 61 KALLAYREKSKAREPDSNAEKPADIRPIDKVTREMAKALVHQFQPHKGYGFDYDK 120
QY 121 DINQWMPVKDNEVRQLHRVQWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQ 180
Db 121 DINQWMPVKDNEVRQLHRVQWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQ 180
QY 181 DNDKFVRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQADYLSHYAEQGN 240
Db 181 DNDKFVRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQADYLSHYAEQGN 240
QY 241 HRLFEAQRNLFAGVSPPEFKDSPRWRQTGISVLNTEIKKQVYADGMQFELSPIYHVAID 300
Db 241 HRLFEAQRNLFAGVSPPEFKDSPRWRQTGISVLNTEIKKQVYADGMQFELSPIYHVAID 300
QY 301 IFLKAYGSAKRVNLEKEFFQSYVQTVENMIMALISISLDPYNTPMFGDSWITDKNFRMAQ 360
Db 301 IFLKAYGSAKRVNLEKEFFQSYVQTVENMIMALISISLDPYNTPMFGDSWITDKNFRMAQ 360
QY 361 FASWARVFPANQAIKYFATDGKQKAPNFKLSNAGFYTFRSKWDKKNATVMVLKASPP 420
Db 361 FASWARVFPANQAIKYFATDGKQKAPNFKLSNAGFYTFRSKWDKKNATVMVLKASPP 420
QY 421 GEHPAQDNGTGFELFIKGRNFTPDAGVYVSGDEAIKMLNWRVQTRIHSITLTDNQNMV 480
Db 421 GEHPAQDNGTGFELFIKGRNFTPDAGVYVSGDEAIKMLNWRVQTRIHSITLTDNQNMV 480
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Db 481 ITKARQNKWETGNLDVLTNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATNGLGVHW 540
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Db 541 QLKEDSNPVFDKTKNRVYTYTRDGNLMIQSLNADRTSLNEEBGKSVYVYNKELKRPFAV 600
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Db 601 FEKPKKNAGTQNFVSIVPYDGGQKAPESIRENKGNDFEKGLNLTITINGKQQLVLVP 659
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RESULT 2

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US-08-900-951-4
; Sequence 4, Application US/08900951
; Patent No. 5919693
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
; APPLICANT: Blain, Francoise
; APPLICANT: Bennett, Clark
; APPLICANT: Gu, Kangfu
; APPLICANT: Zimmermann, Joseph
; APPLICANT: Musil, Roy
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,951
; FILING DATE:
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,639
; FILING DATE: 10 JUNE 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Healey, William J.
; REGISTRATION NUMBER: 36,160
; REFERENCE/DOCKET NUMBER: 104385.116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942 8400
; TELEFAX: (202)942 8484
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 659 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-900-951-4
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Query Match 100.0%; Score 3494; DB 2; Length 659;
Best Local Similarity 100.0%; Pred. No. 4.1e-308;
Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTTKIFKRIIVFAVIALSSGNILAQSSITRKDFDHINLEYSGLKKNKAVAAAGNYDDAA 60
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Db 61 KALLAYREKSKAREPDSNAEKPADIRPIDKVTREMAKALVHQFQPHKGYGFDYDK 120
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Db 121 DINQWMPVKDNEVRQLHRVQWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQ 180
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Db 181 DNDKFVRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQADYLSHYAEQGN 240
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Db 241 HRLFEAQRNLFAGVSPPEFKDSPRWRQTGISVLNTEIKKQVYADGMQFELSPIYHVAID 300
QY 301 IFLKAYGSAKRVNLEKEFFQSYVQTVENMIMALISISLDPYNTPMFGDSWITDKNFRMAQ 360
Db 301 IFLKAYGSAKRVNLEKEFFQSYVQTVENMIMALISISLDPYNTPMFGDSWITDKNFRMAQ 360
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Db 361 FASWARVFPANQAIKYFATDGKQKAPNFKLSNAGFYTFRSKWDKKNATVMVLKASPP 420
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Db 421 GEHPAQDNGTGFELFIKGRNFTPDAGVYVSGDEAIKMLNWRVQTRIHSITLTDNQNMV 480
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Db 481 ITKARQNKWETGNLDVLTNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATNGLGVHW 540
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Db 541 QLKEDSNPVFDKTKNRVYTYTRDGNLMIQSLNADRTSLNEEBGKSVYVYNKELKRPFAV 600
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RESULT 3

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PCT-US95-07391A-4
; Sequence 4, Application PC/TUS9507391A
; GENERAL INFORMATION:
; APPLICANT: IBEX TECHNOLOGIES and
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APPLICANT: ZIMMERMANN, Joseph
 TITLE OF INVENTION: Nucleic Acid Sequences And Expression
 TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
 TITLE OF INVENTION: Flavobacterium heparinum
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hale and Dorr
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington, D.C.
 COUNTRY: U.S.A.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/07391A
 FILING DATE: 09-JUNE-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/258,639
 FILING DATE: 10 JUNE 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Hollie L.
 REGISTRATION NUMBER: 31,321
 REFERENCE/DOCKET NUMBER: 104385.116PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)942-8400
 TELEFAX: (202)942-8484
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 659 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-07391A-4

Query Match 100.0%; Score 3494; DB 5; Length 659;
 Best Local Similarity 100.0%; Pred. No. 4.le-308;
 Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTTKLFKRLIIPAVIALSSGNILAOSSITRKDFDHINLEYSGLEKVNKAVAGNVDAA 60
 Db 1 MTTKLFKRLIIPAVIALSSGNILAOSSITRKDFDHINLEYSGLEKVNKAVAGNVDAA 60
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 Db 61 KALLAYREKSKAREPDFSNAEKPADIRQPIDKVTREMAKALVHQFQPHKGYGFDYCK 120
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 Db 121 DINQWMPVKDNEVPKQLHRVQWQAMALVYHATGDEKYAREWVYQYSDWAEKNPLGLSQ 180
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 Db 181 DNDKFWVRPLEVSDRVQSLPPTFSLFVNSPAPTFPAFLMEFLNSYHQOADYLSTHYAEQGN 240
 QY 241 HRLFEAQRNLFAGVSPFEFKDSPRMRQTGIVSINTEIKQVYADGMPQFELSPIYHVAAD 300
 Db 241 HRLFEAQRNLFAGVSPFEFKDSPRMRQTGIVSINTEIKQVYADGMPQFELSPIYHVAAD 300
 QY 301 IFLKAGSAKRVNLEKEFPQSVQVTVENNIMALISISLDPDYNTPMGDSWIITDKNFRMAQ 360
 Db 301 IFLKAGSAKRVNLEKEFPQSVQVTVENNIMALISISLDPDYNTPMGDSWIITDKNFRMAQ 360
 QY 361 FASWAEVFPANQAIKYFATDGGKQKAPNLFSLKALSNAAGYTFPRSGWKNATVMWLKASPP 420
 Db 361 FASWAEVFPANQAIKYFATDGGKQKAPNLFSLKALSNAAGYTFPRSGWKNATVMWLKASPP 420
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 Db 421 GEFHAQPDNGTTFELFIKGRNFTPDAGVFYVSGDEAIMKLRNRYQTRIHSITLTLNQNMV 480

QY 481 ITKARQNKWETGNNLDVLTYTNPSPYNNLDHORSVLFINKKYFLVIDRAIGATGNLGVHW 540
 Db 481 ITKARQNKWETGNNLDVLTYTNPSPYNNLDHORSVLFINKKYFLVIDRAIGATGNLGVHW 540
 QY 541 OLKEDSNVFDKTKNRVVTYTRDGNLMTQSLNADRTSLNEEGKVSYVYNKELKRPAPV 600
 Db 541 OLKEDSNVFDKTKNRVVTYTRDGNLMTQSLNADRTSLNEEGKVSYVYNKELKRPAPV 600
 QY 601 FEKPKKNAGTQNFVSIYVYDQKAPESIRENKGNDFEKGKLNLTLLTINGKQQLVLP 659
 Db 601 FEKPKKNAGTQNFVSIYVYDQKAPESIRENKGNDFEKGKLNLTLLTINGKQQLVLP 659

RESULT 4
 US-09-134-000C-5302
 ; Sequence 5302, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5302
 ; LENGTH: 649
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-5302

Query Match 4.7%; Score 164; DB 4; Length 649;
 Best Local Similarity 20.1%; Pred. No. 5.4e-06;
 Matches 125; Conservative 91; Mismatches 213; Indels 194; Gaps 31;

QY 120 KDINQWMPVKDNEVPKQLHRVQWQAMALVYHATGDEKYAREWVYQYSDWAEKNPLGLS 179
 Db 70 KEYANRYPDDEPWLFMLSRQSLVDLAQAVALTKERYLQKWSLLIDFI--NDEGEP 127
 QY 180 QNDKFWVRPLEVSDRVQSLPPTFSLFVNSPAPTFPAFLMEFL-----NSVHQOADYLS 232
 Db 128 NSTNRDWRPLDVGIRVTN-----WMKSLYIPIADPRLLGDDVLNNAHLIHLIDYLE 180
 QY 233 THYAEQGNHRLFE-----AQRNLFAGVSPFEFKDSPRMRQTGIVSINTEIKQVYA 283
 Db 181 RSYIDK--YRLSNWGLAIGGMAIDLF---LPELVTS-KQDRLWSRLAEQLDLOFYS 233
 QY 284 DQMQLSPIYHVAADIFLKAYGSAKRVNLEKEFPQSVQVTVENNIMALISISLP----- 339
 Db 234 DGIHWEQSPLY-----QHEVIMTFVYLQ--ISEYLEVQLPDLIR 271
 QY 340 -DYNTPMFGDSWITDKN-----FRMAQFASWAEVFPAN 371
 Db 272 MKLKTPISTHYADNQDILNPDINDSHVNFHYVDIYRKLGFIFEPSWTANRLWTGD 331
 QY 372 -----QAIKYFATDGGKQKAPNLFSLKALSNAAGYTFPRSGWKNATVMWLKASP----- 419
 Db 332 LYEERIWEITMK-----PKEL-----FRG-----ESSGLMAYKAEDIYFTL 366
 QY 420 -----PGEFHAQPDNGTTFELFIKGRNFTPDAGVFYVSGDEAIMKLRNRYQTRIHSITLTL- 474
 Db 367 FNLGHSAGHASTGGFTLQQLQDGLFSDSGRSYVYNKSERLQ-----KECASHNTMFTA 422
 QY 475 DNQNVVITKARONKWTGNNLDVLTYTNPSPYNNLDHORSVLFINKKYFLVIDRAIGATG 534
 Db 423 ENPHTLVS-----DTW-----GYDKL--PTPLFOOI-KELSVGFFAE-----456
 QY 535 NLGVHWQLKEDSNP-VFDKTKNRVVTYTRDGNLMTQSLNADRTSLNEEGKVSYVYN-- 591

Db 457 ---CGWLDKADQNPMEFE---RSFIYKLSINSVVIDSFA-----CQKETEITSTYNLA 504
QY 592 -----KELRRPAFVFEKPKN---AGTQNFVSVIYPDQKAPESIRENK-----GNDF 638
Db 505 PSINCKQEAHRFAUTINKHYKTYLLFAGGQYQOSVA-----KGSEIYNQLNEHPRLSNKF 558
QY 639 --EKGKLNLLTLINGKQOLVNP 659
Db 559 CYTKGKEIQATVISPLEDIOITP 581

RESULT 5
US-09-134-001C-3632
; Sequence 3632, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3632
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3632

Query Match 3.6%; Score 126.5; DB 4; Length 698;
Best Local Similarity 18.6%; Pred. No. 0.015;
Matches 139; Conservative 109; Mismatches 284; Indels 217; Gaps 31;

QY 9 IIVPAVIALSGNLTAAQSSITR--KDFHINLEYSGLEKYNKAVAAAGN-----Y 56
Db 32 VFIFAVLVLLGLYLQIAQGGHYKQLIKNDENIT-----VNESVPRGILDRNGKLV 83
QY 57 DDAKALLAYREKSKAREPDSNAEKPAD-IRQPIDKVTREMAKALVHQFQPHKGYY 115
Db 84 DNASKMSITYTRNKTQSKQEMLTAKKLTDLIKWTDKITER--DK-----127
QY 116 FDYKGINWQWP-----VKONEVRWQLHRV--KWWQA 146
Db 128 ---KDFWIOMYPSFAKKLMRKEQLMLEDSISQDQDPTQLRDKIGKKQLTKKDLQV 183
QY 147 MALV-----YHATGDEKYAREWVYQYSDWARKNPLGLSQDND 183
Db 184 LAIYREMNAGSTLDPQTIKNEVDYSEKAYAVSQSLKLPVNTMTMDRKYPG---DTL 240
QY 184 KFWRRPLEVSDRVQSIPPTSLFVNSPAFTPAFLMEFLNSYHQOADYLSHYABQGNHRL 243
Db 241 RGIFG--DVSTSTEGIPKELT-----EQVLSKGYSRNDRVGRKSYLEYQVEDV 285
QY 244 FEAQNLFAGVSPEPKDSPRWQGTGLSVLNTETIKQVYADGMQFELSPIYHVAADIFL 303
Db 286 LKGTTRQOM---:KVTTKSGRVISSVLPNPSGR-----GHDQLQT-----IDIDL 326
QY 304 KAYGSARVYN--LEKEFFPOSYQVTENVNIMIALISISLPDYNTPMFGDSWITDKNFAQF 361
Db 327 Q-----KKVESLLEKQISKLSRQAGKMDNALMVQNPKNQDILAIAGKQIDKQGLKDY 381
QY 362 --ASWARRVPANQAIAK-YFATDQKQKAPN-----FLSKALSNAGFTYFRSGWDKNA-----410
Db 382 DIGNFTAQYTVGSVKGSTGLLAGYONKAINVGMTMVDPLKFOGGLTKRSYFNKNGHVSI 441
QY 411 -----TMVLKASPPGCFEHAQPDNGTFELFIKGRNFTPDAGVVFVYSGDE 454
Db 442 DDKQALMHSSNVYMFKTALAGDPYTSNGSLNN-----IADAG-----481

QY 455 AIMKLRNWWYQTRIHSHTLTLDNQNMVITKARQNKWETGNMLDVLTYTNPSPYNDLHORSV 514
Db 482 --RKLRLKGLNQVGLGKLTGIDLFPNETPGQIEPLTNFNGNYLDLAIGQYDTVTYPLQLSQYV 539
QY 515 LFNKKYFLV--IDRAIGEATGNLGVHMQLKEDSNVPFQDKTKRNVYTVTYRDGNNMLIQS 571
Db 540 STIANDGYRIQPHIGLSIYESTN-----KQETGPLKKIKGNVLKNVNNNSNDEIKEV 591
QY 572 LNADRTSLNEEGKSVSYVYNKELKRP-----AFVE--KPKKNAGTQNFVSVIYV-- 619
Db 592 QEGFKMAFNEKQG--TGYASPRNTVWPSAGKTGTAEVFQDGEPRVNSYIGVAPVDDPKLS 650
QY 620 ----YDQKAPESISIRENKGNDFEKGLN 644
Db 651 FSIYTYNQPVPPPWML---NGGDLGRDVIN 676

RESULT 6
US-08-258-639A-9
; Sequence 9, Application US/08258639A
; Patent No. 5681733
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
; APPLICANT: Blain, Francoise
; APPLICANT: Bennett, Clark
; APPLICANT: Gu, Kangfu
; APPLICANT: Zimmermann, Joseph
; APPLICANT: Musil, Roy
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,639A
; FILING DATE: 10 JUNE 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Healey, William J.
; REGISTRATION NUMBER: 36,160
; REFERENCE/DOCKET NUMBER: 104385.116
; TELEPHONE: (202)942-8400
; TELEFAX: (202)942-8484
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-258-639A-9

Query Match 3.5%; Score 124; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 VLKASPPGCFEHAQPDNGTFELFI 436
Db 1 VLKASPPGCFEHAQPDNGTFELFI 23

RESULT 7
US-08-900-951-9

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; Sequence 9, Application US/08900951
; Patent No. 5919693
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
; APPLICANT: Blain, Francoise
; APPLICANT: Bennett, Clark
; APPLICANT: Gu, Kangfu
; APPLICANT: Zimmermann, Joseph
; APPLICANT: Musil, Roy
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,639
; FILING DATE: 10 JUNE 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Healey, William J.
; REGISTRATION NUMBER: 36,160
; REFERENCE/DOCKET NUMBER: 104385.116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942 8400
; TELEFAX: (202)942 8484
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-07391A-9
;
; Query Match 3.5%; Score 124; DB 2; Length 23;
; Best Local Similarity 100.0%; Pred. No. 9.3e-05;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 414 VLKASPPGGEFHAQPDNGTFELFI 436
; DB 1 VLKASPPGGEFHAQPDNGTFELFI 23
;
; RESULT 9
; US-08-258-639A-10
; Sequence 10, Application US/08258639A
; Patent No. 5681733
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
; APPLICANT: Blain, Francoise
; APPLICANT: Bennett, Clark
; APPLICANT: Gu, Kangfu
; APPLICANT: Zimmermann, Joseph
; APPLICANT: Musil, Roy
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,639A
; FILING DATE: 10 JUNE 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Healey, William J.
; REGISTRATION NUMBER: 36,160
; REFERENCE/DOCKET NUMBER: 104385.116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942 8400
; TELEFAX: (202)942 8484
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-07391A-9
;
; Query Match 3.5%; Score 124; DB 2; Length 23;
; Best Local Similarity 100.0%; Pred. No. 9.3e-05;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 414 VLKASPPGGEFHAQPDNGTFELFI 436
; DB 1 VLKASPPGGEFHAQPDNGTFELFI 23
;
; RESULT 8
; PCT-US95-07391A-9
; Sequence 9, Application PC/TUS9507391A
; Patent No. 5919693
; GENERAL INFORMATION:
; APPLICANT: IBEX TECHNOLOGIES and
; APPLICANT: ZIMMERMANN, Joseph
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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/ LENGTH: 23 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-258-639A-10
Query Match 3.4%; Score 119; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 0.00026;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 101 KALVHOFQPHKGYGFDYDKDIN 123
Db 1 KALVHFWFPHKGYGFDYDKDIN 23

RESULT 10
US-08-900-951-10
/ Sequence 10, Application US/08900951
/ Patent No. 5919693
/ GENERAL INFORMATION:
/ APPLICANT: Su, Hongsheng
/ APPLICANT: Blain, Francoise
/ APPLICANT: Bennett, Clark
/ APPLICANT: Gu, Kangfu
/ APPLICANT: Zimmermann, Joseph
/ APPLICANT: Musil, Roy
/ TITLE OF INVENTION: Nucleic Acid Sequences And Expression
/ TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
/ TITLE OF INVENTION: Flavobacterium heparinum
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hale and Dorr
/ STREET: 1455 Pennsylvania Avenue, N.W.
/ CITY: Washington, D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC DOS/MS DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/900,951
/ FILING DATE: 10 JUNE 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Healey, William J.
/ REGISTRATION NUMBER: 36,160
/ REFERENCE/DOCKET NUMBER: 104385.116
/ TELEPHONE: (202)942 8400
/ TELEFAX: (202)942 8484
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 23 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-900-951-10
Query Match 3.4%; Score 119; DB 2; Length 23;
Best Local Similarity 91.3%; Pred. No. 0.00026;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 101 KALVHOFQPHKGYGFDYDKDIN 123
Db 1 KALVHFWFPHKGYGFDYDKDIN 23

RESULT 11
US-08-900-951-10
/ Sequence 10, Application US/08900951
/ Patent No. 5919693
/ GENERAL INFORMATION:
/ APPLICANT: Su, Hongsheng
/ APPLICANT: Blain, Francoise
/ APPLICANT: Bennett, Clark
/ APPLICANT: Gu, Kangfu
/ APPLICANT: Zimmermann, Joseph
/ APPLICANT: Musil, Roy
/ TITLE OF INVENTION: Nucleic Acid Sequences And Expression
/ TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
/ TITLE OF INVENTION: Flavobacterium heparinum
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hale and Dorr
/ STREET: 1455 Pennsylvania Avenue, N.W.
/ CITY: Washington, D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC DOS/MS DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/900,951
/ FILING DATE: 10 JUNE 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Healey, William J.
/ REGISTRATION NUMBER: 36,160
/ REFERENCE/DOCKET NUMBER: 104385.116
/ TELEPHONE: (202)942 8400
/ TELEFAX: (202)942 8484
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 23 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-900-951-10
Query Match 3.4%; Score 119; DB 2; Length 23;
Best Local Similarity 91.3%; Pred. No. 0.00026;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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PCT-US95-07391A-10
/ Sequence 10, Application PC/TUS9507391A
/ GENERAL INFORMATION:
/ APPLICANT: IBEX TECHNOLOGIES and
/ APPLICANT: ZIMMERMANN, Joseph
/ TITLE OF INVENTION: Nucleic Acid Sequences And Expression
/ TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
/ TITLE OF INVENTION: Flavobacterium heparinum
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hale and Dorr
/ STREET: 1455 Pennsylvania Avenue, N.W.
/ CITY: Washington, D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/07391A
/ FILING DATE: 09-JUNE-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/258,639
/ FILING DATE: 10 JUNE 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BAKER, Hollie L.
/ REGISTRATION NUMBER: 31,321
/ REFERENCE/DOCKET NUMBER: 104385.116PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)942-8400
/ TELEFAX: (202)942-8484
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 23 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
PCT-US95-07391A-10
Query Match 3.4%; Score 119; DB 5; Length 23;
Best Local Similarity 91.3%; Pred. No. 0.00026;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 101 KALVHOFQPHKGYGFDYDKDIN 123
Db 1 KALVHFWFPHKGYGFDYDKDIN 23

RESULT 12
US-07-973-320-2
/ Sequence 2, Application US/07973320
/ Patent No. 5286486
/ GENERAL INFORMATION:
/ APPLICANT: Payne, Jewel M.
/ APPLICANT: Fu, Jenny M.
/ TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
/ TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David R. Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
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QY 104 VHQFQPHKGYGYD-----YKQDINWQM-----WPKVQNEV----- 134
Db 168 PESIMPEFRVAGYEIPLLTYAQANLHLALLRDLSTLYGDKWGTQNNIBENYNRQKKHI 227
QY 135 -RWQLHRVKKWQA-MALVYHATGDE-----KYAREWVYQYSDWAR-----KNPLGLSDND 183
Db 228 SEYSNHCWKYNSGLSLNGSTYEQWYNRFRREMILMVLDAAPFIYDPRMYSNETS 287
QY 184 KFVWR-----PLEVSDRVQSLPTFTSLFVNSPAPFTAPFLMEFLNSYHQOADIYLSHYAEQ 238
Db 288 TOLTREYVTFDIFSLISNPDIGSFQMENTAFTPLV-----DYLDLYIYT 336
QY 239 GNRHLP--EAQRNLF-----AGVSPPEPKSPRWQTCISVLNTEIKQVYADGMQFELSP 292
Db 337 SKYKASHEIQPDLFYWCVHKVSFKKSEQNLY--TTGI-----YKTSGYISSG 384
QY 293 IYHVAIDIF-----LKAYGSAKRVNLEKEFPQSYVQTVENMIM 331
Db 385 AYSFRGNDIYRTLAAPSVVVVYPTQNYGVQEVGYGVKGHVYRGD--NKYDLYDSIDQ 442
QY 332 -----ALISISLPDYN-----PMFGDSWITDKNFRMAQFASWARVFP 369
Db 443 LPPDGEPIHEKYTHRLCHATAISKSTPDYDNATIPF--SW-----THRSAEY--YNR IYP 494
QY 370 AN---QAIKYFATDGKQG--KAPNLSKALSNAAGFYTFRSGW--DKNATVMVLKASPPG 421
Db 495 NKIKKIPAVKXKLDLSTVKGPGFTGGDLVRG-----SNGYIGDIKATV-----NSPLS 546
QY 422 E-----FHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNMYRQTRIHSTLTLD 475
Db 547 QKZRVVRVATSVSGLFNFI-----VNYDEKEK-----LEKAQKAVNLFTEGRNALQKYTDY 671
QY 476 NQNMVITKARQWET--GNLVDLTY-----TNPSYPN-----LDH--QRSVL 515
Db 568 NDEIALQKQFQSTVETIGEGK-LTYGSGFYIEYSTIOPNPNHPIKTLHLNLSNNSPF 626
QY 516 FINKKYLVIDRAIGATGNLGVHWOLKEDSNFVDTKURVYTVYTDGNNLM--IQSL 572
Db 627 YVDSIEFIPVD-----VNYDEKEK-----LEKAQKAVNLFTEGRNALQKYTDY 671
QY 573 NADRTSL 579
Db 672 KVDQVSI 678
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RESULT 14

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US-08-258-639A-2
; Sequence 2, Application US/08258639A
; Patent No. 5681733
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
; APPLICANT: Blain, Francoise
; APPLICANT: Bennett, Clark
; APPLICANT: Gu, Kangfu
; APPLICANT: Zimmermann, Joseph
; APPLICANT: Musil, Roy
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/258,639A
; FILING DATE: 10 JUNE 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Healey, William J.
; REGISTRATION NUMBER: 36,160
; REFERENCE/DOCKET NUMBER: 104385.116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942-8400
; TELEFAX: (202)942-8484
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 772 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-258-639A-2
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Query Match 3.4%; Score 118; DB 1; Length 772;

Best Local Similarity 20.5%; Pred. No. 0.11; Matches 128; Conservative 79; Mismatches 229; Indels 188; Gaps 30;

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QY 145 QAMALVYHATGDEKYAREWVYQYSD---WARKNPLG--LSQDNDFVWRPLEVSDRV--QS 198
Db 109 ELMALNVLMTKDPKVGREAITSIIDLETATFPAGDISRGIGLFWVTGAIVDWCYDQL 168
QY 199 LPPTFSLFVNS-----PAPTPAFIMEFLNSYHQOADIYLSHYAEQGNHRLFEA 246
Db 169 KPEKTRFRKAFVRLAKMLECGYPPVKDKSIVGHASEWMIMRDLISVGLIAYDE---FPE 225
QY 247 QRLNLAGVSPPEPKDSRW-----RQTGISVLNTEIKQVYA-----DGM 286
Db 226 MYNLAAGREFKEHLVARNWFYPSHNHYHQGMSYLVNFTNDLFALWILDRMGAGVFNPGQ 285
QY 287 QFELSPYIHVAAIDIFLKAYGSAKRVNLEKEFPQSYVQTVENMIMAILISLDPYNTPMF 346
Db 286 QFTLYDAIKRRPDGQILAGGD---VDYSRKPKYYT-----MPALLAGSY--YKDEYL 334
QY 347 GDSWITDKNFRMAQFASWARVFPANQAIKYFATDGKQG--KAPNLSKAL---SNAGFYTF 402
Db 335 NYEFLKDPN-----VEPHCKLFELWRDTQLGSRKPDLDPLSRYSYSGSPFGWMIA 383
QY 403 RSGWCKNATVMVLKASPPGGEF---HAQPDNGTFELFIKGRNFTPDAGVFV--YSGDEAIM 457
Db 384 RTGWGPESVIAEMKN---EYSLNHHQHDAGAFQIYYKG--PLAIDAGSYTSGSSGVNSP 439
QY 458 KLRNMYRQTRIHSTLT-----DNQNMVITKARQ----- 486
Db 440 HNKNPFRKRTIAHNSLLIYDPKETFFSSSGYGGSDHTDFAANDGGQRLPGKGIAPRLKEM 499
QY 487 --NKWETGNL-----DVLTYNPSYPNL-----DHORSVLFINKK----- 520
Db 500 LAGDFRTGKILAQGFDPDQNT---PDYTLKGDITAAYSKAKVEKRSFLEFLMLKDAKVP 556
QY 521 -YFLVIDRAIGBATGNLGVHWOLKEDSNFVFK-----TKNRVTVTVYRDGNN-- 566
Db 557 AAMIVFDKVA-----SNPDFKFKLLHSIEQPEIKGNQITIKRTKNGDS 601
QY 567 -----LMQSLNADRTSLNBEKGVSYY-----NKLKRPAPVFE--KPKK 606
Db 602 GMLVNTALLPDAANSNITSIG--GKGKDFWVFGTNTDPKGTDEALERGERVETPKK 660
QY 607 NAGTQNFVSIYVYDQG--OKAPEI 628
Db 661 AAADYILNVIQIADNTQOKLHEV 684
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RESULT 15

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US-08-900-951-2
; Sequence 2, Application US/08900951
; Patent No. 5919693
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
```


APPLICANT: Blain, Francoise
APPLICANT: Bennett, Clark
APPLICANT: Gu, Kangfu
APPLICANT: Zimmermann, Joseph
APPLICANT: Musil, Roy
TITLE OF INVENTION: Nucleic Acid Sequences And Expression
TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
TITLE OF INVENTION: Flavobacterium heparinum
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,951
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,639
FILING DATE: 10 JUNE 1994
ATTORNEY/AGENT INFORMATION:
NAME: Healey, William J.
REGISTRATION NUMBER: 36,160
REFERENCE/DOCKET NUMBER: 104385.116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)942 8400
TELEFAX: (202)942 8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-900-951-2

Query Match 3.4%; Score 118; DB 2; Length 772;
Best Local Similarity 20.5%; Pred. No. 0.11;
Matches 128; Conservative 79; Mismatches 229; Indels 188; Gaps 30;
QY 145 QAMALVYHATGKXAREWVYQSD---WARKNPLG-LSQDNDKFWVRPLEVSDRV--QS 198
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QY 199 LPPTFSLFVNS-----PAFTPAFLMEFLNSYHQQADYLSHYABQGNHRLPEA 246
DB 169 KPEEKTRFVKAFVRLAKMLECGYPPVKDKSIYGHASEWMIMRDLISVGIAIYDE---PPE 225
QY 247 QNLFAGVSFPEFKDSPW-----RQTGISVLNTEIKKQVYA-----DGM 286
DB 226 MYNLAAGRFKEHLVARNWFFSHNVHQGWSYLNVRFTNDLFALWILDRMGAGNVFNPCQ 285
QY 287 QPELSPYHVAADIFLKAYSKARVNLEKEFPQSYVQTVENMIMALISISLPDYNTPMF 346
DB 286 QFILDYAIYKRRPDGQILLAGD---VDYSRKKPKYTT-----MPALLAGSY--YKDEYL 334
QY 347 GDSWITDKNFRMAQFASWVFPANQAIKYFATDGKQ--KAPNLSKAL---SNAGFYTF 402
DB 335 NYEFLKDPN-----VEPHCKLFEFLWRDTQLGSRKPDLDPLSRYSGPSFGWMIA 383
QY 403 RSGWKNATVMVLKASPGGEF---HAQPDNGTFFELFKGRNFTPDAGVFV--YSGDEAIM 457
DB 384 RTGWGPESVIAEMKNV---EYSLNHHQHQDAGAFQIYYKG--PLAIDAGSYTSSGGYNP 439
QY 458 KLRNMYRQTRIHSITLTL-----DNQNMVITKARQ-----486
DB 440 HKNKFFKRTIAHNSLLIYDPKETSSSGYGGSDHTDFAANDGQRLPGKGIAPRDLKEM 499

QY 487 --NKWETGNNL-----DVLTYTNPSYPNL-----DHQSVLPINKK----- 520
DB 500 LAGDFRTGKILAQGFQPDNQ---PDYTYLKGDTAAYSAKVKEVKRSFLNLLKDAKVP 556
QY 521 -YFLVIDRAIGEATGNLGVHQLKEDSNPVDK-----TKNRVYTYTRDGN-- 566
DB 557 AAMIVFDKVA-----SNPDKKFWLLHSIQEPEIKGNQITIKRTKNGDS 601
QY 567 -----LMIQSLNADRTSLNEEEKVSYVY-----NKKELKRPAPVFE-KPKK 606
DB 602 GMLVNTALLPDAANSNITSIG-GKGKDPWFVTNYTNDPKGTDALRGEWRVEITPKK 660
QY 607 NAGTONFVSIVPYDG--OKAPEI 628
DB 661 AAEDYLNVIQIADNTQOKLHEV 684

Search completed: July 27, 2004, 17:32:01
Job time : 22 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 31, 2004, 15:56:51 ; Search time 993 Seconds
(without alignments)

3253.947 Million cell updates/sec

Title: US-09-802-285A-2

Perfect score: 3494
Sequence: 1 MTTKIFKRIIVFAVIALSSG.....XGKLNLTITNGKQQLVLP 659

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool.p/US09802285/runat_27072004_155105_9097/app.query.fasta_1.839
-DB=Published Applications NA -QFMR=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09802285 @CNCN 1 1 912 @runat_27072004_155105_9097
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2:	/cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/2/pubpna/PTCUS_PUBCOMB.seq:
6:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
7:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
8:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
9:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
10:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
11:	/cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq:
12:	/cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:
13:	/cgn2_6/ptodata/2/pubpna/US09F_PUBCOMB.seq:
14:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
18:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-282-122A-9400

; Sequence 9400, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

1	243	7.0	2688	13	US-10-282-122A-9400	Sequence 9400, Ap
2	176	5.0	3763	13	US-10-158-844-186	Sequence 186, App
c	166.5	4.8	11427	9	US-09-070-927A-165	Sequence 165, App
4	139	4.0	2295	16	US-10-398-221-2467	Sequence 2467, Ap
c	139	4.0	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
6	132.5	3.8	2088	13	US-10-282-122A-34562	Sequence 34562, A
7	130.5	3.7	2043	13	US-10-282-122A-35377	Sequence 35377, A
8	123	3.5	1599	16	US-10-369-493-45761	Sequence 45761, A
9	122.5	3.5	2753	10	US-09-769-736-9	Sequence 9, Appli
10	121	3.5	2541	16	US-10-320-797-2302	Sequence 2302, Ap
11	120	3.4	2034	16	US-10-369-493-46899	Sequence 46899, A
12	118.5	3.4	1737	16	US-10-369-493-26002	Sequence 26002, A
13	118.5	3.4	1737	16	US-10-369-493-26008	Sequence 26008, A
14	118	3.4	7787	16	US-10-398-221-3883	Sequence 3883, Ap
15	117.5	3.4	4455	13	US-10-335-977-4204	Sequence 4204, Ap
16	117.5	3.4	8709	13	US-10-282-122A-22858	Sequence 22858, A
17	116	3.3	2757	13	US-10-282-122A-34553	Sequence 34553, A
c	116	3.3	4702	8	US-08-781-986A-268	Sequence 268, App
c	116	3.3	4702	13	US-10-329-824-268	Sequence 268, App
19	116	3.3	14121	10	US-09-802-840-31	Sequence 31, Appli
20	116	3.3	14121	10	US-09-920-033-3	Sequence 31, Appli
21	116	3.3	14121	13	US-10-403-902A-31	Sequence 31, Appli
22	116	3.3	14121	13	US-10-147-196-3	Sequence 3, Appli
23	116	3.3	14121	16	US-10-388-263-545	Sequence 545, App
24	116	3.3	2961	13	US-10-282-122A-12261	Sequence 12261, A
25	115.5	3.3	3945	16	US-10-369-493-25219	Sequence 25219, A
26	115.5	3.3	3945	9	US-09-801-368-369	Sequence 369, App
27	115.5	3.3	3996	9	US-10-398-221-10	Sequence 10, Appl
28	115.5	3.3	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
29	115.5	3.3	3222	9	US-09-974-300-2654	Sequence 2654, Ap
30	115	3.3	16535	13	US-10-158-844-74	Sequence 74, Appli
c	115	3.3	1830121	15	US-10-329-960-1	Sequence 1, Appli
c	115	3.3	1830121	16	US-10-329-960-1	Sequence 1, Appli
33	114.5	3.3	3903	10	US-09-882-227-387	Sequence 387, App
34	114.5	3.3	1830121	15	US-10-329-960-1	Sequence 1, Appli
35	114.5	3.3	1830121	16	US-10-329-960-1	Sequence 1, Appli
36	114.5	3.3	1830121	15	US-10-329-960-1	Sequence 1, Appli
37	114	3.3	2613	16	US-10-369-493-37158	Sequence 37158, A
38	114	3.3	6702	13	US-10-282-122A-10381	Sequence 10381, A
39	113.5	3.2	4765	13	US-09-841-553-7	Sequence 7, Appli
40	113.5	3.2	4765	14	US-10-090-624-5	Sequence 5, Appli
41	112.5	3.2	6720	9	US-09-070-927A-321	Sequence 321, App
42	111.5	3.2	2889	13	US-10-282-122A-41762	Sequence 41762, A
43	111	3.2	2169	16	US-10-369-493-34629	Sequence 34629, A
44	111	3.2	2253	9	US-09-993-292A-19	Sequence 19, Appl
45	111	3.2	8908	9	US-09-993-292A-18	Sequence 18, Appl

; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9400
 ; LENGTH: 2688
 ; TYPE: DNA
 ; ORGANISM: Bacillus anthracis
 ; US-10-282-122A-9400

Alignment Scores:

Pred. No.: 4,83e-17 Length: 2688
 Score: 243.00 Matches: 132
 Percent Similarity: 37.82% Conservatives: 93
 Best Local Similarity: 22.18% Mismatches: 250
 Query Match: 6.95% Indels: 120
 DB: 13 Gaps: 29

US-09-802-285A-2 (1-659) x US-10-282-122A-9400 (1-2688)

QY	277	IlleLysLysGlnValTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHisVal	296
Db	622	TTTGAAAGAGTCTTTACTGAAGAGGGGTTTCATAAGGAGCATTCACCATCTTATCATTTA	681
QY	297	AlaAlaIleAspIlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeuGluLys	316
Db	682	-----TTAGTAGCTTCTAATATCAAGAGGTTAGCAAACTGGATGAAA	723
QY	317	GlupheProGlnSerTyrValGlnThrValGluAsnMetIleMetAla	332
Db	724	GAATTCGATAAGGAA--GTAAGTTTGATTTTAAATAAGATTTATAAAAAACAGAGAG	780
QY	333	---LeuIleSerIleSerLeuProAspTyrAsnThrProMetPheGlyAspSerTyr	350
Db	781	TATGCCATACATATCATCTCGTCAGATGGTCTTACCACCAATATGTGATCGCAAGCA	840
QY	351	---IleThrAspLysAsnPheArgMetAlaGlnPheAlaSerTrpAlaArgValPhePro	369
Db	841	AATTTAGTGGGAATAATTATAAG-----GATTATATGAG	876
QY	370	AlaAsnGlnAlaIleLysTyrPheAlaThrAspGlyLysGlnGlyLysAlaProAsnPhe	389
Db	877	AGTCATCAGTATCTT--TATGTAGTTACTAAGGCAAAAGGAAAGCCCTACAGAA	933
QY	390	LeuSerLysAlaLeuSerAsnAlaGlyPheTyrThrPheArgSerGlyTrpAspLys	408
Db	934	GATGATAAGGTATTTCTCTAAATCAGGTATGCAATCTTTAGGAATGATTCGAGTAAGAA	993
QY	409	---AsnAlaThrValMetValLeuLysAlaSerProGlyGluPheHisAlaGlnPro	427
Db	994	GAGAAGGCTACTATGTTTATTATACAGCTGCTTATCATCATAGTACCATACATAGCATAGT	1053
QY	428	AspAsnGlyThrPheGluLeuPheIleLysGlyArgAsnPheThrProAspAlaGlyVal	447
Db	1054	GAT-----GATTTAAATTTA	1068
QY	448	PheValTyrSerGlyAspGluAlaIleMetLysLeu---ArgAsnTrpTyrArg	464
Db	1069	TATATTATTCAAATCGTGAATATTACAGAAGCGGGTCTTAATAGATATAATTATAA	1128
QY	465	-----GlnThrArgIleHisSerThrLeuThrLeuAspAsn	476
Db	1129	GATCCTTTTACTGAATATCGTATTTCATCTATTGCTCATATAACATCATGTTGTACGGA	1188
QY	477	GlnAsnMetValIleThrLysAlaArgGlnAsnLys-----TrpGluThr	491
Db	1189	AAAGGGTTACCTAGAACTCATCGTCAGTAGTAAAGAAAGTCTATTATTCAGATTATGAATC	1248
QY	492	GlyAsnAsnLeuAspValLeuThrTyrThrAsnProSerTyrProAsnLeuAspHisGln	511
Db	1249	AACAAGATAAAGTTGAAGCGGCGGAATTAATTACGTTTATACAGGTGTGACATAGT	1308
QY	512	ArgSerValLeuPheIleAsnLysLysTyrPheLeuValIle---AspArgAlaIleGly	530
Db	1309	CGTACTGTAAAGTTACATGAAGAGCAAGAAATAAGTAGTAGGAGGATTGGTGAATCT	1368
QY	531	GluAlaThrGlyAsnLeuGlyValHisTrpGlnLeuLysGluAspSerAsnProValPhe	550
Db	1369	GATAAACGTCATGAATATTAAGTTATTATGGCATGTTTCATCAGAT-----ATTACA	1419
QY	551	AspLysThrLysAsnArgValTyrThrTyrArgAspGlyAsnLeuMetIleGln	570
Db	1420	GTACATGTAAGAGATCGTATTCTTGAGTTATTTCGTAAACCAACCAAGTAATGGAAATG	1479
QY	571	SerLeu-----AsnAlaAspArgThrSerLeuAsnGluGlu---GluGlyLys	585
Db	1480	GAAGTAACCTACAGTTACTGGTGTATATACGAGCATTAATATGAACAAACAAAGCCCTCAG	1539
QY	586	ValSerTyrValTyrAsnLysGluLeuLysArgProAlaPheValPheGluLysProLys	605
Db	1540	GTGAGT-----GGCTGGGTATTTCCAAAAATGGGG	1569
QY	606	LysAsnAlaGlyThrGlnAsnPheValSerIleValTyrProTyrAspGlyGlnLysAla	625

QY	113	TyrGlyTyrPheAspTyrGlyLysAspIleAsnTrpGlnMetTrpProValLysAspAsn	132
Db	139	TTTCGGAAGTAGTTCATATCTTAATTTAAATTAACCTGG-----AAT	177
QY	133	GluValArgTrpGln-----LeuHisArgValLysTrpTrpGlnAlaMet	147
Db	178	GRACAAAGAGACGGGGATATTTAAGATTAAATACAGGTCATACGTTTATAGCATGCTTA	237
QY	148	AlaLeuValTyrHisAlaThrGlyAspGluLysTyrAlaArgGluTrpValTyrGlnTyr	167
Db	238	ATAGCCCGTATAATCATCTGTTGATATCAAGATATATAAAAAATCTATAGAGTTAAAT	297
QY	168	SerAspTrpAlaArgLysAsnProLeuGlyLeuSerGlnAspAsnAspLysPheValTrp	187
Db	298	AAAGATTGATTAATAATCATTCATTTGAACITTCACCAACATTCATGCTTTT-----	351
QY	188	ArgProLeuGluValSerAspArgValGlnSerLeuProThrPheSerLeuPheVal	207
Db	352	-----CATGATGAAACTACAGCGCTA-----CGTCTACAGTATTGGTTA	390
QY	208	AsnSerProAlaPheThrProAlaPheLeuMetGlu-----PheLeuAsn	222
Db	391	AGATTCTACATTTTACAGCTCAAGTGTATACAGGAGAGAAATATATTGTTAGAAAAA	450
QY	223	SerTyrHisGlnAlaAspTyrLeuSerThrHisTyr-----AlaGluGlnGlyAsn	240
Db	451	AGTATGGAAGATACTCGCAAACTTTTATCAGAGGACTTTTTCATGCTACTAATAACAAT	510
QY	241	HisArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLys	260
Db	511	CATGGTATGTTTCAA---GATAGAGCGCTACTTACTTATGTCATCGTAT-----TTTAAA	561
QY	261	---AspSerPro-----ArgTrpArgGlnThrGlyIleSerValLeuAsnThrGlu	276
Db	562	GGAGAAATCCTTCCTTGGAAAAATATATAAAGTTGGCTGTACACGTTTAAAGGATTAT	621

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Db 1570 GAAAAACGAGTGCT-----ACAACAATTGAGGTGGACATTAGGTTCTTAATGTA 1620
      ::: ||| ::::|
Qy 626 ProGluIleSerIleArgGluAsnLysGlyAsnAspPheGluLysGlyLys----- 642
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Db 1621 GAG-----TGATACAGAGTTTCGATGAAGGATTTTAAATTAGGTAGACGANTTG 1674
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 643 -----LeuAsnLeuThrLeuThrIleAsnGlyLysGlnGlnLeu 655
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1675 ATTCCTTAATTTAGAGAAAACATTCAGAGAGTACACGTAATTTA 1719
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RESULT 2
US-10-158-844-186/c
; Sequence 186, Application US/10158844
; Publication No. US20040029118A1
; GENERAL INFORMATION:
; APPLICANT: Kunsch et al.
; TITLE OF INVENTION: Streptococcus pneumoniae polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: Dell Latitude Pentium 3
; OPERATING SYSTEM: Windows 98
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/158,844
; FILING DATE: 03-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/961,527
; FILING DATE: 1997-10-30
; APPLICATION NUMBER: US 60/029,960
; FILING DATE: 1996-10-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Mark J.
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB340PID1
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-10-158-844-186

Alignment Scores:
Pred. No.: 4.8e-09 Length: 3763
Score: 176.00 Matches: 116
Percent Similarity: 34.63% Conservative: 80
Best Local Similarity: 20.49% Mismatches: 231
Query Match: 5.04% Indels: 140
DB: 13 Gaps: 20

US-09-802-285A-2 (1-659) x US-10-158-844-186 (1-3763)
Qy 71 SerLysAlaArgGluProAspPheSerAsnAlaGluLysProAlaAspIleArgGlnPro 90
Db 2173 TCAAAAGACTATGAGAAAGTCAAGAGTTCCCTTGAACGCTTGATGCACAATCGTTTATG 2114
Qy 91 IleAspLysValThrArgGluMetAlaAspLysAlaLeuValHisGlnPheGlnProHis 110
Db 2113 TTGTATAGT---CCTTGGGATATGGAGCCTTGTTCAAAAATCCATCAAAATCCAGCG--- 2060
Qy 111 LysGlyTyrGlyTyrPheAspTyrGlyLysAspIleAsnTyrGlnMetTyrProValLys 130
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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Db 2059 -----ATCGTATGGGATCAAGTATTTTGAAGAT 2033
Qy 131 AspAsnGluValArgTyrGlnLeuHisArgValLysTyrTrpGlnAlaMetAlaLeuVal 150
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Db 2032 GATCCAGAATGGTCTTATATGCTCAATCGACAAGAATATCTCTTCAGCTTTATGATAGGG 1973
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 151 TyrHisAlaThrGlyAspGluLysTyrAlaArg-----GluTyr 163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1972 TATCTGTAGAAGGAGATAAGGACTATATTCAAAAGTCGAAGTCTCTTTCTATTCTATG 1913
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 164 ValTyrGlnTyrSerAspTyrAlaArgLysAsnProLeuGlyLeuSerGlnAspAsnAsp 183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1912 ATTGAGCAGGTGAGAGAAATTTTCTCCTCAATCCTTGATGACTAGAACCTTGATACGGGT 1853
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Qy 184 -----LysPheValTyrArgProLeuGluValSerAspArgValGlnSerLeuProPro 201
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1852 ATTCGTTCTTTACITGTTGAAACTA----- 1826
Qy 202 ThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMetGluPheLeu 221
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1825 ---CTCTTGTCTCTCTCTGAAATTTGACTGTCTAGAGAGAAAGAACTAGAGAAATTTG 1769
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 222 AsnSerTyrHisGlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGln----- 238
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Db 1768 GTCAGTCTAGAAAAGCAGATTGACTTTATGAAAAGCTACTATCGCGCCCAAGTACACCTT 1709
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Qy 239 GlyAsnHisArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSerProGlu 258
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Db 1708 AGTAACTGGGGATTTTACAAACAATTCGATGCTTCTATCTATCATCTCTTTTCAGAT 1649
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Qy 259 PheLysAspSerProArgTyrArgGlnThrGlyIleSerValLeuAsnThrGluLys 278
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Db 1648 AAGATGGATCTAGAAGAAGCTTACCATTGTCTTCAGAGGAGTTGAAACAGCAAAATGAG 1589
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Qy 279 LysGlnValTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHisVal----- 296
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1588 ACACAGATTTTAGGAGATGGAAGCCAGTTTGAACAGTCGATTCCTCTATCATGTAGAGTT 1529
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Qy 297 -----AlaAlaIleAspIlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeu 314
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1528 TATAAAGCCTTGCTGGAATTTGTGCTC-----TTG 1499
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Qy 315 GluLysGluPheProGlnSerTyrValGlnThrValGluAsnMetIleMetAlaLeuIle 334
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1498 CTTCCAGACTTGCAGAGATAGTTTACCAAGATGTCTGGGAAAGATGCGCACTATATTCAA 1439
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Qy 335 SerIleSerLeuProAspTyrAsnThrProMetPheGlyAspSerTyrIleThrAspLys 354
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1438 ATGATGACAGGCTTAGATGACGGACTTTGGCTTTTGGTGTAGCGATCTTACAGAAACG 1379
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 355 AsnPheArgMetAlaGlnPheAla----- 362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1378 ACAGAAATTTTGAGCCTGTCTGCTGTGTTTGAACACGAGAGACCTTCTTAAACGGTCTG 1319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 363 -----SerTyrAlaArgValPheProAlaAsnGlnAlaIleLysTyrPhe 377
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1318 GATGTTAAAGTTGATTTGCTTAGCCTCTCTGTTCTGGGGCGGAGAAAGGTCAAGCGACTG 1259
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 378 AlaThrAspGlyLysGlnGlyLysAlaProAsnPheLeuSerLysAlaLeuSerAsnAla 397
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1258 CAGGAATTTGAAAAGAGAGCTTGGCAGCCTAAG-----TCCATGATCTTTGAAGACTCT 1205
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 398 GlyPheTyrThrPheArgSerGlyTyrAspLysAsnAlaThrValMetValLeuLysAla 417
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1204 GGACATGTCTGCAATTAAGGAT-----GAACATCGTTATCTATTTTCAAAAT 1157
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 418 SerProGlyGluPheHisAlaGlnProAspAsnGlyThrPheGluLeuPheIleLys 437
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1156 GGTCCGCTAGGAAGTCCCATAGTCATAGTACAGAGATAGTTTTTGTTCAGATATCAA 1097
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 438 GlyArgAsnPheThrProAspAlaGlyValPheValTyrSerGlyAspGluAlaIleMet 457
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1096 GSCCAACCTATTTTCATAGATCTGGCGTTATTCTTATTCG--GGAGATATATGAACGTTA 1038
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

QY 458 LysLeuArgAsnTrpTyrArgGlnThrArgIleHisSerThrLeuThrLeuAspAsnGln 477
Db 1037 TCCTCTAAAGAGGCTGGAGTCATTCGACTGCAATGT-----999
QY 478 AsnMetValIleThrLysAlaArgGlnAsnLysTrpGlu--ThrGlyAsnAsnLeuAsp 496
Db 998 -----AGATGGGAAGCTCCGGAAGATCACGGG 969
QY 497 ValLeu-ThrTyr-----500
Db 968 ATCTGTGGAATATGAATACTATCTCCTCCTCCTGTTTGTACCATTAAGAAAGGAGGG 909
QY 501 -----ThrAsnProSerTyrProAsnLeuAspHi 510
Db 908 AGTGCAATATATGAGGGGCTTATGTGTGAGCAAGAACCTGATTTGCTTATCTTT--CA 852
QY 510 sGlnArgSerValLeuPheIleAsnLysLysTyrPheLeuValIleAsp-----ArgAl 528
Db 851 CAGGAGAAATCTCATGTGTGGTAGAGGATGCTGGCTCTTGGTAGATGACATCAGGTG 792
QY 528 alleGlyGluAlaThrGlyAsnLeuGlyValHisTrpGlnLeuLysGluAspSerAsnPr 548
Db 791 TCAAGGTCAA-----CATGAGGTGTGACTCAGTTT-----761
QY 548 ovalPheAspLysThrLysAsnArgValTyrThrTyrArgAspGly-----AsnAs 566
Db 760 -ATCCTTGCAAGGAT-----GTGACCTATCAAGATGGGAAATCAATCA 717
QY 566 nLeuMetIleGlnSer 571
Db 716 GTTGAGACTATGGAGT 701

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RESULT 3

```

US-09-070-927A-165/c
; Sequence 165, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;             Steven Barash
;             Patrick J. Dillon
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512

```

```

; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-070-927A-165

```

```

Alignment Scores:
Pred. No.: 3.54e-07 Length: 11427
Score: 166.50 Matches: 121
Percent Similarity: 35.18% Conservative: 89
Best Local Similarity: 20.27% Mismatches: 215
Query Match: 4.77% Indels: 174
DB: 9 Gaps: 26

US-09-802-285A-2 (1-659) x US-09-070-927A-165 (1-11427)
QY 120 LysAspIleAsnTrpGlnMetTrpProValLysAspAsnGluValArgTrpGlnLeuHis 139
Db 7871 AAAGAGTATCGTGGGATCGGTATCCTCGATGATCCAGATCGCTCTTTTGTGTGAGT 7812
QY 140 ArgValLysTrpTrpGlnAlaMetAlaLeuValTyrHisAlaThrGlyAspGluLysTyr 159
Db 7811 CGTCAAGCTTCTTGTAGATCTGGCACAAAGCATATGCACTTCTAAAAAAGAACGTTAC 7752
QY 160 AlaArgGluTrpValTyrGlnTyrSerAspTrpAlaArgLysAsnProLeuGlyLeuSer 179
Db 7751 TTACAGAAATGGCACAGCTTGCTTATTGATTATT-----AACGATGAGGCTGAGCCA 7698
QY 180 GlnAspAsnAspLysPheValTrpArgProLeuGluValSerAspArgValGlnSerLeu 199
Db 7697 AATTCGACGAATAGGAGTGTTCGCGCTTGTAGATTCGGGATTCGAGTAACAAAC-- 7641
QY 200 ProProThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMetGlu 219
Db 7640 -----TGGATGAAGAGCTTGACGTATATTCATTCGCTGATTTTCTGAGT 7599
QY 220 PheLeu-----AsnSerTyrHisGlnGlnAlaAspTyrLeuSer 232
Db 7598 CTATTAGGAATTCATGATGTTTGAACACACGCTTCTGTATCCATCTCGGACTATTTCGAG 7539
QY 233 ThrHisTyrAlaGluGlnGlyAsnHisArgLeuPheGlu-----245
Db 7538 CGTCTCTATATCGATAAA-----TACAGCTCAGTAATTGGGGTGTGTGGCAATTGGT 7485
QY 246 -----AlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLysAspSerPro 263
Db 7484 GGAATGCGACTATTGATTATT-----CTTCCAGAACTGGTGACACAGT--- 7440
QY 264 ArgTrpArgGlnThrGlyLysSerValLeuAsnThrGluLysLysGlnValTyrAla 283
Db 7439 AAACAGAGGATCTAATATGCTCGTTTGTAGCTGAACAGCTTGTATCAAAATCTATTCA 7380
QY 284 AspGlyMetGlnPheGluLeuSerProIleTyrHisValAlaAlaIleAspIlePheLeu 303
Db 7379 GATGGAATTCATGGGAGCAGCCCGCTGTAC-----7347
QY 304 LysAlaTyrGlySerAlaLysArgValAsnLeuGluLysGluPheProGlnSerTyrVal 323
Db 7346 -----CAGCAGAAAGTTTGTATGATGACATTCGTG 7320
QY 324 GlnThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuPro-----339
Db 7319 TATCTATTGCG-----ATTCTGAATATCTTGAAGTCCAGTACCATTAGATCTTCGC 7266
QY 340 ---AspTyrAsnThrProMetPheGlyAspSerTrpIleThrAspLys-----354
Db 7265 ATGAAATTAACACCTATTCTTCTACCCATTATTGGCGGATAACCAAGATATCCTA 7206
QY 355 -----AsnPhe-----356

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```
Db 7205 AATCCGATCAATGATGATGATCATGTCACACTTTTCATTACGTATATGATATATCGCAAA 7146
QY 357 -----
Db 7145 TTAGGTTTCATATTGGAACCTCCATGACTCGGATATGGCAAGGCTT-----TGGAGC 7092
QY 366 -----
Db 7091 GGGGATCTTTTGAAGAAAGATCTGGGAAC-AATGAAGCCAAAGAACTTTTCGTGG 7033
QY 379 -----
Db 7032 CGAATCAAGTGGCGTGATGGCGTACAAAGCAGA-----GGATATCTA----- 6991
QY 395 SerAsnAlaGlyPheThrPhe---ArgSerGlyTyrAspLysAsnAlaThrValMet 413
Db 6990 -----TTTACATTTTAAACGGTCTGCATGG----- 6964
QY 414 ValLeuLysAlaSerProProGlyGlu-PheHisAlaGlnProAspAsnGlyThrPheGl 433
Db 6963 -----GAGCGCACATGCTCATGCTTCTACAGGTGGATTTTAC 6928
QY 433 uLeuPheIleLysGlyArgAsnPheThrProAspAlaGlyValPheValTyrSerGlyAs 453
Db 6927 ACTCAACTACAGGGGATGACTTTATTTTCCGATAGTGTGCTGTACAGCTATGTCACAA 6869
QY 453 pGluAlaIleMetLysLeuArgAsnTyrPtyrArgGlnThrArgIleHisSerThrLeuTh 473
Db 6867 ATCAGAGCGACTTCAGCTA-----AAAGAGTGGCGTTCGCACAAATACGATGTT 6820
QY 473 rLeu---AspAsnGlnAsnMetValIleThr-----LysAlaArgGl 486
Db 6819 TATCGCAGAAAATCCCACTACTTTAGTTTCCGATACGTGGGGTTATGACAAATACCGAC 6760
QY 486 nAsnLysTrpGluThrGlyAsnAsnLeuAspValLeuThrTyrThrAsnProSerTyrPr 506
Db 6759 ACCCTTATTTTCAGCAAAATAAAGAACTTCTCTCGGTTTTTTTTCGAGATGCGGCTGGCT 6700
QY 506 oAsnLeuAspHisGlnArgSerValPhePheIleAsnLysLysTyrPheLeu----- 523
Db 6699 GGATANGCGGATCAGATCCATCGATTTTTCAGCGCAGCTTCATCTATTAAAGTCGAT 6640
QY 524 -----ValIleAspArgAlaIleGlyGlu-----AlaTh 533
Db 6639 CAACCTCCGTAGTATTATTATGATGCTTTTCAGGACAGCAAGAGACTGAAATTTACGAGTAC 6580
QY 533 rGlyAsnLeuGlyValHisTrpGlnLeuLysGluAspSerAsnProValPheAspLysTh 553
Db 6579 CTATATTTTGGCACCGTCGATAAATGTGCAAAAGAGCGCATCGGTTTGTCTTTAACTAC 6520
QY 553 rLysAsnArgValTyrThrTyrArgAspGlyAsnAsnLeuMetIleGlnSerLeuAs 573
Db 6519 GAACACAGCATAGTACACACTCTTTTCTGCTGAGGC----- 6483
QY 573 nAlaAspArgThrSerLeuAsnGluGluGlyLysValSerTyrValTyrAsnLysGl 593
Db 6482 -----CAACACAGCAATCATGTCGCAAAAAGGTTTCAGAGATTATAACACAGCT 6436
QY 593 uLeuLysArgPro-----AlaPheValPheGluLysProLysLysAsnAlaGl 609
Db 6435 GAATGAGCCACCGCTTATCAACAAGTTTGTTCACAAACGGG-AAAGAAATTCAG 6377
QY 609 yThrGlnAsnPheValSerIleValTyrProTyrAspGlyGlnLysAla 625
Db 6376 CAACAGTCATTCTCCGTTAGAGGATATCCAAATTAACGCAATAAAAGT 6328
```

RESULT 4

```
US-10-398-221-2467
; Sequence 2467, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
```

```
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2467
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2467
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Alignment Scores:

Pred. No.:	4,25e-05	Length:	2295
Score:	139.00	Matches:	148
Percent Similarity:	31.94%	Conservative:	97
Best Local Similarity:	19.30%	Mismatches:	280
Query Match:	3.98%	Indels:	242
DB:	16	Gaps:	37

US-09-802-285A-2 (1-659) x US-10-398-221-2467 (1-2295)

```
QY 7 LysArgIleIle-----ValPheAlaValIle-----AlaLeuSerSerGly 20
Db 4 AAAGAATATATCTGTATTCTGTCATTTTCTGTTTCTACTGGGATTTGTTAGCCCATTC 63
QY 21 AsnIleLeuAlaGlnSerSerSerIleThrArgLysAspPheAspHisIleAsnLeuGlu 40
Db 64 ACAATTAAGCAAGTGCAGCAACCAATAACAATAAATTAACATTGTGAAGAGCTT----- 114
QY 41 TyrSerGlyLeuGluLysValAsnLysAlaValAlaAlaGlyAsnTyrAspAlaAla 60
Db 115 -----TATCGAAGACTAAA 129
QY 61 LysAlaLeu---LeuAlaTyrTyrArgGluLysSerLysAlaArgGluProAspPheSer 79
Db 130 AAACATTTAGGTAAACCATATTCCGACAGCAGGACAGAGAGAGAGGCGCAATTACTTTC 189
QY 80 AsnAla-----GluLysProAlaAspIleArgGlnPro--- 90
Db 190 GACTGCTCAGGTACACACAATATGTTATGAAAAGTAAACAGAGATGAAGAATTCCTAAT 249
QY 91 -----IleAspLysValThrArgGluMetAlaAspLysAla 102
Db 250 ACTTCAGCTCCTCAATATTTCAGTCTGCTGATAAAGTGAAAAATGGTAATCAAAAACTGGT 309
QY 103 LeuValHisGlnPheGlnProHisLysGlyTyrGlyTyrPheAspTyrGlyLysAspIle 122
Db 310 GATTTAGTATATTTCAAAAGGTCATGTAGGAATA---TACATAGGTAATGGTAAAAATGATT 366
QY 123 AsnTrpGlnMetTrpProValLysAspAsnGluValAlaGTrpGlnLeuHisArgValLys 142
Db 367 AATGCTCAAAATGATGGAGTCAAAATAGACAACATT-----AATAGTAGT 411
QY 143 TrpTrpGlnAlaMetAlaLeuValTyr-----HisAlaThrGlyAspGluLysTyrAla 160
Db 412 TATTCGCAGAGTATTTTGTGGATACGGAAGATTTTCAATTTCTCCGAGAAAAAGGA 471
QY 161 ArgGluTrpValTyrGlnTyrSerAsp-----Trp----- 170
Db 472 TCTAAATCCGCTATGCTGTGTGCAGATTTAAATTTACGATCTAGCAATAAATCGGATAGT 531
QY 171 -----AlaArgLysAsnProLeuGly-----LeuSerGlnAspAsnAspLys 184
Db 532 TCAGTAGCTGGAAAAAGTTCCCAACGCGCTAAAGATATCTATTCAGCTTAGACAGTATAG 591
QY 185 PheValTrpArgProLeuGluValSerAspArgValGlnSerLeuProThrPheSer 204
Db 592 AATGGTTGGTGTGTGTAACATTATATAATAACTAAAGGTTATATGTTTAAATACAATAAT 651
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```
QY 205 LeuPheValAsnSerProAlaPheThrProAlaPhe----- 216
Db 652 TATTCTCCGATACACCTGTGATAAAACATACCTATGCCAAGGATAATATAAAGTTAAGA 711
QY 216 ----- 216
Db 712 ACGAAACCAATGGGTAGATAGTGTAGTCAAAAGCTACAAAAGGTGAAAAAGTTACT 771
QY 217 -----LeuMetGluPheLeuAsnSerTyrHisGlnGlnAlaSerTyrLeuSerThrHis 234
Db 772 GTGAACCTTAAACTAATGTGAATGGTGTGTATCAAGTAAACATACGCGGAAAAACAGGC 831
QY 235 TyrAlaGluGlnGlyAsnHisArgLeuPheGluAlaGlnArgAsnLeu-----PheAla 252
Db 832 TATATGATTAAATAATAATTAATCTAGTAGAATAATCCCTTGATATGGAAACGTATTAT 891
QY 253 GlyValSerPheProGluPheLeuAspSerProArgTyrPheGlnThrGlyIleSerVal 272
Db 892 GCGGTGGTACCTTAATCTCGGTAGTCGACAACTGG--GATAGTAGCATTAGCTTA 948
QY 273 LeuAsnThrGlu-----IleLysLysGlnValTyrAlaaspGlyMetGlnPheGlu 289
Db 949 GTGTGACCAAGCAGAGCTGTAAAGTAGAA-----ATGGATACAAAT 993
QY 290 LeuSerProIleTyrHisValAla----- 297
Db 994 AGTGGTCTTGGTATAAGTAACATATCAAAACCAACAGGTATACCCACCTAACAGAT 1053
QY 298 -----AlaIleAspIlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeu 314
Db 1054 GATTATTATCCAAACACTACTGTCTTAAACAGCTATTACGCTAAAGATAATTTAAACCTA 1113
QY 315 GluLysGlu-----PheProGlnSerTyrValGlnThrValGlu-----AsnMetIle 330
Db 1114 AGAACAAAGCAACTTGGGTAGCGAGCTTGGCTCAAAAAGTACAAAAGGTGAAAAAGTA 1173
QY 331 MetAlaLeuIleSerIleSerLeuProAspTyrAsnThrProMetPheGly----- 347
Db 1174 ACAGTTAAATTTAAACAAAGTAAATGGTGGTATCATCAAGTAACCTATGCTGGTAAAAAA 1233
QY 348 -----AspSerTyrIleThrAspLysAsnPheArgMetAlaGlnPhe 361
Db 1234 GGTTCATGATCTTAAATGATAACTATTATAGTCGAAAAGCGCTTAATATGAAACCTAT 1293
QY 362 -----AlaSerTrp-----AlaArg 366
Db 1294 TATGCGGTGAGTAGCTTAATTTACGTAGTGAGCGGAATGGGATAGTAGCATAGTCAAA 1353
QY 367 ValPheProAlaAsnGlnAlaIleLys-----TyrPhe 377
Db 1354 GTGGTCCAGAGGTAGAGCTGTCAAAAGTCGAAATGGACACGAATGTGGCAATTTGGTTT 1413
QY 378 AlaThr-----AspGlyLysGlnGlyLysAlaPro-----AsnPheLeuSerLys 392
Db 1414 AAGTAGCACTTACATAAATCAACAGGTATATCCCACTAAATGATTATATATTTATCTGAA 1473
QY 393 AlaLeuSerAsnAlaGlyPheTyrThr-----PheArgSerGly 405
Db 1474 ACGCGTGTCTTAAAAACCTATTATGCAAAAGATAATTTAACTTACGTAGCGAAGCAAA 1533
QY 406 TrpAspLysAsnAlaThrValMetValLeuLysAlaSerProProGlyGluPheHisAla 425
Db 1534 TGGGATAGTAGAGTTACTCAAAAGTAGAAAAAGGTGAAAAAGTAAACAGTCAATTCGAAA 1593
QY 426 GlnProAspAsnGlyThrPheGluLeuPheIleLysGlyArgAsnPheThrProAspAla 445
Db 1594 ACAAGTATCGATGCTGTATGAAGTA----- 1620
QY 446 GlyValPheValTyrSerGlyAspGluAlaIleMetLysLeuArgAsnTrpTyrArgGln 465
Db 1621 -----ACATACGGTGTGTAAGAAAGGCTATATGATTTTAAATAATAATTAT----- 1665
```

```
QY 466 ThrArgIleHisSerThrLeuThrLeuAspAsnGlnAsnMetVal-----IleThrLys 483
Db 1666 ---CTGTAGCAGAACCACTAGATTTGAAAAACATATTACGAGTTAACACATTAAATTTA 1722
QY 484 AlaArgGlnAsnLysTrpGluThrGly----- 492
Db 1723 CGTAGTGAATCTAAATGGGACAGCAGCATAAAGCAAGTGGTACCTGAAGCGCTAAAGTA 1782
QY 493 -----AsnAsnLeuAspValLeuThrTyrThrAsnProSer 504
Db 1783 AAAAGTTGAAATGAACACACAGTGAATTTGGTACAAAGTAACCTATCAAAATAAAACA 1842
QY 505 -----TyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsnLysLysTyrPhe 522
Db 1843 GGTATATGCGCTAAATGATTATATTTATCTGAAACTGCTGTGTAAAACTTATAT 1902
QY 523 LeuValIleAspArgAlaIleGlyGluAlaThrGlyAsnLeuGlyValHisTrpGlnLeu 542
Db 1903 -----GCAAAAGATAATTTAAACTTACGTAGCGAAGCA 1935
QY 543 LysGluAspSerAsnProValPheAspLysThrLysAsnArgValTyrThrTyrArg 562
Db 1936 AAATGGGATAGT-----GAAATTTCTCAAGTAGTAGAA 1968
QY 563 AspGlyAsnAsnLeuMetIleGlnSerLeuAsnAlaAspArgThrSerLeuAsn----- 580
Db 1969 AAAGGTCAAAAGTAACCTATTATTCG-----AAACCAAGTATAAATGGTTGG 2016
QY 581 -----GluGluGluGlyLysValSerTyrValTyrAsnLysGluLeuLysArgPro 597
Db 2017 CATCAAGTAACCTTACGCTGTGTAATAAAAGGTTATATG-----ATTTTAAAGTGAT 2064
QY 598 AlaPheValPheGluLysPro 604
Db 2065 AACTATTATTGCGAAAAACCA 2085
RESULT 5
US-10-398-221-2058/c
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2058
Alignment Scores:
Pred. No.: 3.82 Length: 3011208
Score: 139.00 Matches: 148
Percent Similarity: 31.94% Conservative: 97
Best Local Similarity: 19.30% Mismatches: 280
Query Match: 3.98% Indels: 242
DB: 16 Gaps: 37
US-09-802-285A-2 (1-659) x US-10-398-221-2058 (1-3011208)
QY 7 LysArgIleIle-----ValPheAlaValIle-----AlaLeuSerSerGly 20
Db 2117803 AAAAGATTATATCTCTGATTGTCATTTTGTCTTGTACTGGGATGTTTACCCCATTC 2117744
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```
Qy 21 AsnIleuAlaGlnSerSerSerIleThrArgLysAspPheAspHisIleAsnLeuGlu 40
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117743 ACAATTAAAGCAAGTCAGCAACCAATACAAATACAAATTTGAAGAGCTT----- 2117693
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 41 TyrSerGlyLeuGluLysValAsnLysAlaValAlaGlyAsnTyrAspAlaala 60
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117692 -----TATGCAGAGCTTAA 2117678
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 61 LysAlaLeu-----LeuAlaTyrArgGluLysSerLysAlaArgGluProAspPheSer 79
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117677 AAAATTTAGTTAAACCATATTCGACAGCAGGACAGAGAGGCGCCAAATTTACTTTC 2117618
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 80 AsnAla-----GluLysProAlaAspIleArgGlnPro--- 90
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117617 GACTGCTCAGGTTACACACATATGTTTATGAAAAAGTAAACAGGAGTAAGAATTCCTAAT 2117558
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 91 -----IleAspLysValThrArgGluMetAlaAspLysAla 102
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117557 ACTTCAGCTCCTCAATATTCAGCTGCTGATTAAGTAAAAAATGGTAATCAAAAACCTGGT 2117498
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 103 LeuValHisGlnPheGlnProHisLysGlyTyrGlyTyrPheAspTyrGlyLysAspIle 122
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117497 GATTTAGTATATTTCAAAGGTCATGTAGGAATA--TACATAGGTAATGGTAAAAATGATT 2117441
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 123 AsnTrpGlnMetTrpProValLysAspAsnGluValArgTrpGlnLeuHisArgValLys 142
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117440 AATGCTCAAAATGATGGAGTCAAAATAGACACATT-----AATAGTAGT 2117396
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 143 TrpTrpGlnAlaMetAlaLeuValTyr-----HisAlaThrGlyAspGluLysTyrAla 160
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117395 TATTGGCAGAGATTTTTTGTGGATACGGAAGATTTTCAATTTCCGAGAAAAAAGGA 2117336
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 161 ArgGluTrpValTyrGlnTyrSerAsp-----Trp----- 170
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117335 TCTAAATCGGCTATGCTGTGTGCAGATTTAAATTTACGATCTAGCAATAAATCGGATAGT 2117276
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 171 -----AlaArgLysAsnProLeuGly-----LeuSerGlnAspAsnAspLys 184
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117275 TCAGTAGCTGGAAGAAAGTTCCCAAGGCGCTAAAGTATCTATTGACTTAGACAGTATAG 2117216
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 185 PheValTrpArgProLeuGluValSerAspArgValGlnSerLeuProProThrPheSer 204
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117215 AATGGTTGGTGATGCTTAATTAATAATACTAAAGGTATATGTGTTAAATACAACTAAT 2117156
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 205 LeuPheValAsnSerProAlaPheThrProAlaPhe----- 216
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117155 TATTTCGATACACCTGTGATAAAACATATCTATGCCAAGGATAATATATAAATAAGA 2117096
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 216 ----- 216
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Db 2117095 ACGAAAGCAACATGGGATAGCGATGTAGCTCAAAAAGTACAAAAAGGTGAAAAAGTTACT 2117036
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 217 -----LeuMetGluPheLeuAsnSerTyrHisGlnGlnAlaAspTyrLeuSerThrHis 234
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2117035 GTGAACCTTAAACATAATGTGTAATGGTTGGTATCAAGTAACATACGCGGAAAAACAGGC 2116976
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 235 TyrAlaGluGlnGlyAsnHisArgLeuPheGluAlaGlnArgAsnLeu-----PheAla 252
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2116975 TATATGATTTTAAATAATAATTAATTAATCTAGTAGAAAAATCCCTGGAATATGGAAACGTATTAT 2116916
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 253 GlyValSerPheProGluPheLysAspSerProArgTrpArgGlnThrGlyIleSerVal 272
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2116915 GCGGTTGGTACCTTAAATCTGCGTAGTCGACCAAACTGG---GATAGTAGCATTAGCTTA 2116859
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 273 LeuAsnThrGlu-----IleLysLysGlnValTyrAlaAspGlyMetGlnPheGlu 289
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2116858 GTGTACCGAAGCGAGAGCTGTAAAGTAGAA-----ATGATACAAAT 2116814
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 290 LeuSerProIleTyrHisValAla----- 297
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
Db 2116813 AGTGGTCTCTTGGTATAAAGTAACATATCAAAACCAACAGGTTTACATCCCACTAACAGAT 2116754
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|

Qy 298 -----AlaIleAspIlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeu 314
||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:| ||| ||| :|:|:|:|:|
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Db 2115790 CATGAAGTAACTTACGGTGTGTAAGGTTATATG-----ATTTTAAGTGAT 2115743

QY 598 AlapheValPheGluLysPro 604

Db 2115742 AACTATTAGTCGAAACCA 2115722

RESULT 6

US-10-282-122A-34562

; Sequence 34562, Application US/10282122A

; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; PRIORITY FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 34562

; LENGTH: 2088

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-10-282-122A-34562

Alignment Scores:

Pred. No.:	0.000207	Length:	2088
Score:	132.50	Matches:	140
Percent Similarity:	34.59%	Conservative:	108
Best Local Similarity:	19.53%	Mismatches:	260
Query Match:	3.79%	Indels:	210
DB:	13	Gaps:	30

US-09-802-285A-2 (1-659) x US-10-282-122A-34562 (1-2088)

QY 9 IleIleValPheAlaValIleAlaLeuSerSerGlyAsnIle---LeuAlaGlnSerSer 27

Db 88 GTATTATCTTCTGCTATAGTCGGATTAGGTTATTATACAAATAGCACAAAGGATCT 147

QY 28 SerIleThrArg-----LysAspPheAspHisIleAsnLeuGluTyrSerGlyLeuGlu 45

Db 148 CATTACAAACAATTATCAAAACGATGAACNTAACT----- 186

QY 46 LysValAsnLysAlaValAlaAlaGlyAsn-----Tyr 56

Db 187 ---GTTAATGAATCAGTACCAAGAGCGCAATACTAGATAGAAATGCAAAAGTACTAGTT 243

QY 57 AspAspAlaAlaLysAlaLeuLeuAlaTyrTyrArgGluLysSerLysAlaArgGluPro 76

Db 244 GATAATGCTTCAAGATGCTTATTACATACACAGAACCGTAAACATCACAAGAGAA 303

QY 77 AspPheSerAsnAlaGluLysProAlaAsp---IleArgGlnProIleAspLysValThr 95

Db 304 ATGTTAAATACTGCTAAGAAACTCACAGATTTTAAATAATGGATACAGATAAAATACT 363

QY 96 ArgGluMetAlaAspLysAlaLeuValHisGlnPheGlnProHisLysGlyTyrGlyTyr 115

Db 364 GAGAGA-----GATAAA----- 375

QY 116 PheAspTyrGlyLysAspIleAsnTyrGlnMetTyrPro-----ValLysAspAsn 132

Db 376 -----AAGGATTTTGGATTCAAAATGATCCGTCATCTGCTAAAAAGTT-AAT 422

QY 133 GluValArgTyrGlnLeuHisArgValLysTyrTyrGln----- 145

Db 423 GAGAAAAGA-----ACAATTAATGTTAGAGGATGCGAGTATTTTCAACAGACCAATTTGA 476

QY 146 -----AlaMet 147

Db 477 TACCCAACTTAGAGATAAAATAGGAAAAACAATTAACACAGTTAACTAAAAAGATTT 536

QY 148 AlaLeuValTyrHisAlaThrGlyAspGluLysTyrAla----- 160

Db 537 GCAAGTTTACCAATTTATCGGGAATGAACGCTGGTCAACTCTAGATCCTCAACAAT 596

QY 161 -----ArgGlu----- 162

Db 597 TAAAAATGAAGACGTAAAGCGAGAAAGAATATGCGCGGTATCAACAGAGCTTTCTAAAT 656

QY 163 ---TyrValTyrGlnTyrSer-AspTyrAlaArgLysAsnProLeuGlyLeuSerGlnAs 181

Db 657 ACCTGGTAAATACATACAAATGATGGGATGGAATAACCCATACCGT-----GA 707

QY 181 pAsnAspLysPheValTyrArgProLeuGluValSerAspArgValGlnSerLeuProPr 201

Db 708 TACTTTAAGAGGCATATTTGGA-----GATGTGTGCGACTTCGACTGAAGGTATACCTAA 761

QY 201 oThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMetGluPheLe 221

Db 762 AGAATTAACCT-----GAACAATATTT 782

QY 221 uAsnSerTyrHisGlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGlyAsnHi 241

Db 783 ATCAAAAGGTTATTACGAAATGATCGGTCGTAATCTTTATCTTGAATATCAATACGA 842

QY 241 sArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLysAs 261

Db 843 AGATGTTCTTAAAGGCACGAGAAACAATG-----AAATATACAAC 884

QY 261 pSerProArgTyrArgGlnThrGlyIleSerValLeuAsnThrGluIleLysGlnVa 281

Db 885 TGATAAATCTGGAAGAGTAATAAGTTCAAGAGTACTTAATCTCTGGCTCAAGA----- 936

QY 281 lTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHisValAlaAlaIleAspIl 301

Db 937 -----GGTCATGATTTACAATTACT-----ATAGATAT 965

QY 301 ePheLeuLysAlaTyrGlySerAlaLysArgValAsn-----LeuGluLysGluPhePr 319

Db 966 TGATTTTACAG-----AAAAAGTAGAATCTTTATTAGAAAAACAAATTTTC 1010

QY 319 oGlnSerTyrValGlnThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuPr 339

Db 1011 TAAATTCAGTAGTCAGGTGCTAAGGATATGCAATGCGTTAATGTTGTCCTCAAAATTC 1070

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Qy 339 oAspTyrAsnThrProMetPheGlyAspSerTrpIleThrAspLysAsnPheArgMetAl 359
Db 1071 TAAAAATGGAGACATCTCTCGCTATTGTCAGGAAGCAAAATTGATAAGCAAGGTAAACTCAA 1130
Qy 359 aGlnPhe-----AlaSerTrpAlaArgValPheProAlaAsnGlnAlaIleLys---Ty 376
Db 1131 AGATTATGATTCGGCACTTTACAGCTCAATACAGTACAGTGGTCTTCAGTAAAGGAGG 1190
Qy 376 rPheAlaThrAspGlyLysGlnGlyLysAlaProAsn-----PheLeuSerLy 392
Db 1191 AACATTATTAGTCGATACCAAAATAAAGCTATTAACTGTGGAGAAACTATGGTAGATGA 1250
Qy 392 sAlaLeuSerAsnAlaGlyPheTyThrPheArgSerGlyTrpAspLysAsnAla----- 410
Db 1251 GCCATTAAATTCCAAGGTGGTTTAACTAAGCGTTCTTATTATTAATAAATAATGTCATGT 1310
Qy 411 -----ThrVa 412
Db 1311 ATCTATCGATATAAACAGCACCTTATGCTATCATCAAAAGTATACATGTTTAAACCGC 1370
Qy 412 lMetValLeuLysAlaSerProProGlyGluPheHisAlaGlnProAspAsnGlyThrPh 432
Db 1371 ACTTAAATTAGCAGTGACCCCTATACCTTACAGTATGCTATTACCTAATAAT----- 1422
Qy 432 eGluLeuPheIleLysGlyArgAsnPheThrProAspAlaGlyValPheValTyrSerGl 452
Db 1423 -----ATAGCAGATGCTGT----- 1437
Qy 452 yAspGluAlaIleMetLysLeuArgAsnTrpTyrArgGlnThrArgIleHisSerThrLe 472
Db 1438 -----CGTAAATTCGCTAAAGGTTAAATCAAGTAGTCTTGGCTTAAAC 1484
Qy 472 uThrLeuAspAsnGlnAsnMetValIleThrLysAlaArgGlnAsnLysTrpGluThrGl 492
Db 1485 AGGTATTGACTTACCGAAGCAAGCCAGGCCAAATAGAACCTTAACTAATAATCTCTGG 1544
Qy 492 yAsnAsnLeuAspValLeuThrTyrThrAsnProSerTyrProAsnLeuAspHisGlnAr 512
Db 1545 TAACATTATTAGCTTATGCTATTGGACAATACAGACATATACACCACCTTCAGTTGTCCCA 1604
Qy 512 gSerValLeuPheIleAsnLysLysTyrPheLeuVal-----IleAspArgAlaIle 529
Db 1605 ATACGTATCAACTATGCTAATGCTATGCTATAGAAATCAACCACATATGGATTGCTAT 1664
Qy 529 eGlyGluAlaThrGlyAsnLeuGlyValHisTrpGlnLeuLysGluAspSerAsnProVa 549
Db 1665 TTATGAATCTACTAAT-----AAAGATGAAGCAAGGTACAGGTTATGCTAG 1700
Qy 549 lPheAspLysThrLysAsnArgValTyrThrTyrArgAspGlyAsnAsnLeuMetIl 569
Db 1701 AAACGTAAATTAAGGTATATGTTTAAATAGTAAATTAACCTCAATATGACGAATTA 1760
Qy 569 eGlnSerLeuAsnAlaAspArgThrSerLeuAsnGluGluGlyLysValSerTyrV 589
Db 1761 AGAAGTTCAAGAGGCTTCAAAATGCTTCAATGAAAGCAAGGTACAGGTTATGCTAG 1820
Qy 589 al-----TyrAsnLysGluLeuLysArgProAlaPheValPheGluLysP 604
Db 1821 TTTTGAATAACTGTAGTACCTTCAGCTGGTAAACAGCAAGTCTGTAAGTTTTCAGA 1880
Qy 604 roLysLysAsnAlaGlyThrGlnAsnPheValSerIleValTyrPro 619
Db 1881 CGGAGAACCTAGAGTTAACTCAACAT---ATATCGGTATGACCCCG 1924
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RESULT 7

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US-10-282-122A-35377
; Sequence 35377, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
```

```
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35377
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35377
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Alignment Scores:

Pred. No.:	0.000342	Length:	2043
Score:	130.50	Matches:	134
Percent Similarity:	33.08%	Conservative:	88
Best Local Similarity:	19.97%	Mismatches:	256
Query Match:	3.73%	Indels:	193
DB:	13	Gaps:	27

US-09-802-285A-2 (1-659) x US-10-282-122A-35377 (1-2043)

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Qy 9 IleIleValPheAlaValIleAlaLeuSerSerGlyAsnIle---LeuAlaGlnSerSer 27
Db 88 GTAGTTATATTGGAAATTATAGTTTAAAGTTAGGATATTACAAATTCGCAAGGCTCC 147
Qy 28 SerIleThrArgLysAspPheAspHisIleAsnLeuGluTyrSerGlyLeuGluLys--- 46
Db 148 -----CAATACAGCCAACTAGTTTAAAC 171
Qy 47 -----ValAsnLysAlaValAlaAlaGlyAsn----- 55
Db 172 GATGNAACATAACTGTAAATGAATCTCTTCTAGGGGAAGNAATTCCTGATAGGAATGA 231
Qy 56 -----TyrAspAspAlaAlaLysAlaLeuLeuAlaTyrTyrArgGluLysSerLys 72
Db 232 AAAGTATTAGTAGATAATAGCTTCTTAAACTAAACGATTATACACAAAGATCTAGGAACA 291
Qy 73 AlaArgGluProAspPheSerAsnAlaGluLysProAlaAsp---IleArgGlnProIle 91
Db 292 AGTCAAAAGATATGCTCGATATCTGCAAAAAAATTTGTCATCTCTCTATTACTATGAAACT 351
Qy 92 AspLysValThrArg----- 96
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352 GACAAAATTACTGAAAGAGATAAACAAGATTTTGGATTTCAGAAACACCAAGATGAGTA 411
QY
97 -----GluMetAlaAspLysAlaLeuValHisGlnPheGln 108
Db
412 GACAAATTAATGAAAAAGAACTTCAATGTTAAATGAAGGTAGTATTACCAAGATCAA 471
QY
109 ProHisLysGly----- 112
Db
472 TATGATAACAATATATAAAGAGTTGGAGACAAACAATAATAGTTTATCAAAAAA 531
QY
113 -----TyrGlyTyrPheAspTyrGlyLysAspIleAsnTrpGln 125
Db
532 GACTTACGAGCTTTAGCAATTTATCGTGAATGCTGCTGCTTCTACCATGACCGCAA 591
QY
126 MetTrpProValLysAsnGluValArgTrpGlnLeuHisArgValLysTrpTrpGln 145
Db
592 -----ACAAATTAAGATGAGGATGTAAGTGAATAA----- 621
QY
146 AlaMetAlaLeuValTyrHisAlaThrGlyAspGluLysTyrAlaArgGluTrpValTyr 165
Db
622 -----CAATATGCTGCAGTGTCAACAACCTTATGATGCTTCAGGTGTAAT 669
QY
166 GlnTyrSerAspTrpAlaArgLysAsnProLeuGlyLeuSerGlnAspAsnLysPhe 185
Db
670 ACAACTATGATGGGACCGACGCTATCTTATGTT----- 705
QY
186 ValTrpArgProLeuGluValSerAspArgValGlnSerLeuProProThrPheSerLeu 205
Db
706 -----GATACATTAAAGAGTATA-----TTTGGTAGT 732
QY
206 PheValAsnSerProAlaPheThrProAlaPheLeuMetGluPheLeuAsnSerTyrHis 225
Db
733 GTATCTACATCAAGTGAAGTATCTCTAAGAATTGACCGAA----- 774
QY
226 GlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGlyAsnHisArgLeuPheGlu 245
Db
775 -----CAATATTAGCTAAAGGTTATCT----- 798
QY
246 AlaGlnArgAsnLeuPheAlaGlyValSerPheProGlu-----PheLysAsnSerPro 263
Db
799 -----CGGAATGATGAGTTGGTAAATCCTATTAGAGTATCAATATGAAGATATTTA 852
QY
264 ArgTrpArgGlnThrGlyIle-----SerValLeuAsnThr 275
Db
853 CGTGGTAAGAAAAAGAAATGAATATCTACTGATAAATCTGAAAGATCAATAACTCT 912
QY
276 Glu-----IleLysLysGlnValTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyr 294
Db
913 GAAGTCATTAAATCCTGGATCTAGAGCGGATGATTACAGTTA----- 954
QY
295 HisValAlaAlaIleAspIlePheLeuLysAlaTyrGlySerAlaLysArgValAsn--- 313
Db
955 -----ACAATTTGATAGACTTACAG-----AAGAAAGTAGAATCT 990
QY
314 ---LeuGluLysGluPheProGlnSerTyrValGlnThrValGluAsnMetIleMetAla 332
Db
991 TTATTAGAAAAATCAAAATCAAGACGTTACGCGAGTCAAGGTCTAAAGATATGATAACGG 1050
QY
333 LeuIleSerIleSerLeuProAspTyrAsnThrProMetPheGlyAspSerTrpIleThr 352
Db
1051 CTTATTGTGTGCAAAATCCTAAAAATGGCGATATTTTAGCTATGGCAGGAAACAAATC 1110
QY
353 AspLysAsnPheArgMetAlaGlnPhe-----AlaSerTrpAlaArgValPheProAla 370
Db
1111 GATAAAATGGTAAAGCTAACAGATATGATTTAGGGAACCTTTACTGTCATTTGCAGTT 1170
QY
371 AsnGlnAlaIleLys-----TyrPheAlaThrAspGlyLysGln 383
Db
1171 GGTCTCTTCAGTAAAGAGGTGGAACCTTATTAGCTGGATATCAAAATATGCGATTAAAGTT 1230
QY
384 GlyLysAlaProAsnPheLeuSerLysAlaLeuSerAsnAlaGlyPheTyrThrPheArg 403
Db
1231 GCGCAG-----GAAATGATAGATGAGCCACTTCATTTAAAGGTGGATTAAACAGCGC 1284

QY 404 SerGlyTrpAspLysAsnAlaThrValMetValLeuLysAlaSerProProGlyGluPhe 423
Db 1285 TCCTACTTTAATAAATAAATGATAAAGTCAGAAAT-----AATGATAAA 1326
QY 424 HisAlaGlnProAspAsnGlyThrPheGluLeuPheIleLysGlyArgAsnPheThrPro 443
Db 1327 GAAGCAATTAATGACACTCTTCAAAACGATATATATGTTT-----AAAACGTCTTTAAA 1377
QY 444 AspAlaGlyValPheValTyrSerGly-----AspGluAlaIle 456
Db 1378 TTATCCGGAGATCCTTACTATATAGTGGATGGCTTACCTACAGATATAAGTGAAGCTGGC 1437
QY 457 MetLysLeuArgAsnTrpTyrArgGlnThrArgIleHisSerThrLeuThrLeuAspAsn 476
Db 1438 CAGAAATTAAGAAAAAGGGCTTAATCAAGTCGGATTCGGAGTTTAAACAGGATATTGACTTG 1497
QY 477 GlnAsnMetValIleThrLysAlaArgGlnAsnLysTrpGluThrGlyAsnAsnLeuAsp 496
Db 1498 CCAATTAACAACATAGTCAATTTGAACCATTAACAACAATTCAGGCAATTTATCTGAT 1557
QY 497 ValLeuThrTyrThrAsnProSerTyrProAsnLeuAspHisGlnArgSerValLeuPhe 516
Db 1558 TTATCAATTTGGTCAATATGACACATATAGTCCAAATTCATATACACAGTACGTTCTTACA 1617
QY 517 IleAsnLysLysTyrPheLeuVal-----IleAspArgAlaIleGlyGluAlaThr 533
Db 1618 ATAGCTAATGATGGTTATAGAAATTCACACCAATTTGGATTAGCAATTCATGATGCTACA 1677
QY 534 GlyAsnLeuGlyValHisTrpGlnLeuLysGluAspSerAsnProValPheAspLysThr 553
Db 1678 AATAGT-----GATGACATAGTCCAGTTAAACAAAAAAT 1713
QY 554 LysAsnArgValTyrThrTyrArgAspGlyAsnAsnLeuMetIleGlnSerLeuAsn 573
Db 1714 AAAGGCAATGCTCTTAAACAAAGTAATAATTCAGAAGATCAAAATTAAGAAGTACAAAAA 1773
QY 574 AlaAspArgThrSerLeuAsnGluGluGly 584
Db 1774 GGATTTGAAATGGCATTCATTAAGAAAGATGGA 1806

RESULT 8
US-10-369-493-45761
; Sequence 45761, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 45761
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-45761

Alignment Scores:
Pred. No.: 0.00171 Length: 1599
Score: 123.00 Matches: 109
Percent Similarity: 32.01% Conservative: 76
Best Local Similarity: 18.86% Mismatches: 179
Query Match: 3.52% Indels: 214
DB: 16 Gaps: 31

US-09-802-285A-2 (1-659) x US-10-369-493-45761 (1-1599)

Qy	94	ValThrArgGluMetAlaAspLysAlaLeuValHisGlnPheGlnProHisLysGlyTyr	111
Db	61	ATGCAAAACGAAATAGCGATAGACCTTTGGTCCAC---TTACACACCCAAACAAAGGCGT	117
Qy	114	-----GlyTyr-PheAspTyrGlyLysAspIleAsnTrpGlnMetTrp---	127
Db	118	ATGAATGACCCAAATGGGTGTGGTACGATGAAAAGATGCCAAATGGCATCTGACTTTT	177
Qy	128	ProValLysAspAsnGluValArgTrpGlnLeuHisArgValLysTrpTrpGlnAlaMet	147
Db	178	CAATACACCCAAATGACACCGTATGG-----GGTACGCCATTGTTTGGGGC-----	225
Qy	148	AlaLeuValTyrHisAlaThrGlyAspGluLysTyrAlaArgGluTrpValTyrGlnTyr	167
Db	226	-----CATGCTACTTCCGATGAT-----TTG	246
Qy	168	SerAspTrpAlaArgLysAsnProLeuGlyLeuSerGlnAspAsnAspLysPheValTrp	187
Db	247	ACTAATTGG---GAAGATCAACCCATTGCTATCGCTCCCAAGCGTAAAC-----	291
Qy	188	ArgProLeuGluValSerAspArgValGlnSerLeuProProThrPheSerLeuPheVal	207
Db	291	-----	291
Qy	208	AsnSerProAlaPheThrProAlaPheLeuMetGluPhe-----	220
Db	292	GATTACAGTGCTTCTCTGGCTCCATGGGTGGTTGATTACACACACGAGTGGGTTTTC	351
Qy	221	-----LeuAsnSerTyrHis	225
Db	352	AATGATACTATTGATCCAAAGACAAAGATGCGTTGCGATTTGGACTTATAACACTCCTGAA	411
Qy	226	GlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGlyAsnHisArgLeuPheGlu	245
Db	412	AGTGAAGACCAATACATTAGC-----TATTCTCTGTGATGGTGTACACTTTTACTGAA	465
Qy	246	AlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLysAsp-----	261
Db	466	TACCAAAAGAACCTGTTTACTGCCAACTCCACTCAATTCAGATGCCAAGGTGTC	525
Qy	262	-----SerProArgTrpArgGlnThrGlyIleSerValLeuAsnThrGluIle	277
Db	526	TGGTATGAACCTTCATAAAATGGATATTAGACG-----GCTGCCAAATACAAAGACTAC	579
Qy	278	LysLysGlnValTyrAlaAsp-----	284
Db	580	AAAAATTGAAATTACTCTCTGATGACTTGAAGTCTCTGGAAGCTAGAACTGCAATTGGCC	639
Qy	285	-----GlyMetGlnPheGluLeu-----	290
Db	640	AATGAAGGTTTCTTAGGCTACCAATACGAAATGCCAGGTTGATTGAAGTCCCACTGAG	699
Qy	291	-----SerProIleTyrHisValAlaAlaIleAspIle-----	301
Db	700	CAAGATCCTTCCAAATCTATTGGGTCACTGTTTATTCTATCAACCCAGGTGCACCTGCT	759
Qy	302	-----PheLeuLysAlaTyr	306
Db	760	GGCGGTTCCTTCAACCAATATTTTTGTGGATCCTTCAATGGTACTCATTTTGAAGCGTTT	819
Qy	307	GlySerAlaLysArgValAsnLeuGluLysGluPheProGlnSerTyr-----ValGln	324
Db	820	GACAAATCAATCTAGAGTG-----GTAGATTTTGGTAAGGACTACTATGCTCTTGCAA	870
Qy	325	ThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuProAspTyrAsnThrPro	344
Db	871	ACTTCTCTTCAAC-----ACTGACCCCACTTACGGTTCAGCA	906
Qy	345	MetPheGlyAspSerTrpIleThrAspLysAsnPheArgMetAlaGlnPheAla-----	362
Db	907	TTA---GGTATTGCTCTGGCGTTCA-----AACTGGGAGTACAGTGCCTTTGTCCTCAACT	957

Qy	363	-----SerTrpAlaArgValPheProAlaAsnGlnAlaIleIys	375
			:::
Db	958	AACCCATCGGAGATCATCATGCTCTTTGGTCGCGCAAGTTTTCTTTGGAAC-----ACTGAA	1011
			:::
Qy	376	TyrPheAla-----ThrAspGlyLysGlnGlyLysAlaProAsnPheLeuSerIys	392
Db	1012	TATCAAGCTAATCCAGAGACTGAATTGATCAATTTGAAGCCGCAACCAATTATTGAAC---	1068
Qy	393	AlaLeuSerAsnAlaGlyPheTyrThrPheArgSerGlyTirpAspLysAsnAlaThrVal	412
		:::	:::
Db	1069	---ATTAGTAATGCTGGT-----CCCTGGTCTCGTTTGGTACTACTAAC	1107
			:::
Qy	413	MetValLeuLysAlaSerProGlyGluPheHisGlnProAspAsnGlyThrPhe	432
			:::
Db	1108	ACAACCTTCACTAAGGCCCAATCTTCAATGTCGATTTGAGCACTCGACTGGTACCCTTA	1167
			:::
Qy	433	GluLeuPheIleLysGlyArgAsnPheThrProAspAlaGlyValPheValTyrSerGly	452
Db	1168	GAGTTTGAGTTG-----GTTTAGCGTGTTTAAACACC	1197
			:::
Qy	453	AspGluAlaIleMetLys-----LeuArgAsnTrpTyrArgGlnThrArg	467
		:::	:::
Db	1198	ACACAAACCATATCCAAATCGCTCTTTGCCGACTTATCACCTTTGGTTCAAGGGTTTGA	1257
			:::
Qy	468	-----IleHisSerThrLeuThrLeuAsp	475
Db	1258	GATCCTGAAGAATATTGAGAATGGTGTTTGAACTCAGTGGCTCTCTCTCTTTTGGAC	1317
			:::
Qy	476	AsnGlnAsnMetValIleThrLysAlaArgGlnAsnLysTirpGluThrGly-----	492
			:::
Db	1318	CGTGTTAACTCTAAGGTCCAAGTTTGTCAAGGAGAACCCATATTTTCAACAAACAGAATGCT	1377
			:::
Qy	493	---AsnAsnLeuAspValLeuThrTyrThrAsnProSerTyrProAsn-----	507
Db	1378	GTCACAAACCAACCATTCACAGTCTTGAGAACGACCTAAGTTACTATAAAGTGTACGGCCTA	1437
			:::
Qy	508	LeuAspHisGlnArgSerValLeuPheIleAsn-----LysIys	520
			:::
Db	1438	CTGGATCAAAACATCTTGGAAATTGTACTTCAACGATGGAGATGTGGTTTCTTCAAAATACC	1497
			:::
Qy	521	TyrPheLeuValIleAspArgAlaIleGlyGluAlaThrGlyAsnLeuGlyVal	538
			:::
Db	1498	TACTTCATGACACACCGGTAAACGCTCTAGGATCTGTGAACATGACACCATCGGTGTC	1551
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RESULT 9

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US-09-763-9
; Sequence 9, Application US/09769736
; Publication NO. US20030138775A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21089wo
; CURRENT APPLICATION NUMBER: US/09/769,736
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: GB 9816335.5
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125163
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatenIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3753
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-09-769-9

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Alignment Scores:		
Pred. No.:	0.00759	Length:
Score:	122.50	Matches:
		3753
		160

Percent Similarity:	32.91%	Conservative:	98
Best Local Similarity:	20.41%	Mismatches:	296
Query Match:	3.51%	Indels:	230
DB:	10	Gaps:	37
US-09-802-285A-2 (1-659) x US-09-769-736-9 (1-3753)			
QY	24	AlaGlnSerSerSerIleThrArgLysAspPheAsp	-----HisIleAsnLeu 39
DB	1303	AGTAAATCTCTTTAATATCAAGCGGACTTTAATCTCTAAACAGGTCATTTCAATATA	1362
QY	40	GluTyrSerGlyLeuGluLysValAsnLysAlaValAlaAlaGlyAsnTyrAspAla 59	
DB	1363	TCCTATAATGGT-----AACAAATGCACGACAGGCAATCTTCG---GAATTT 1407	
QY	60	AlaLysAlaLeuLeuLeuAlaTyrTyrArgGluLysSerLysAlaArgGluProAspPheSer 79	
DB	1408	AAAGACCAACTTTATGCTTATAGTGGAAATTTAGGTGCAGTCTCTCAATCAAGATGGTTCA 1467	
QY	80	AsnAlaGluLysProAlaAspIleArgGlnPro---IleAspLysValThrArgGluMet 98	
DB	1468	AAAGTTGAA-----GCCAGCCTCTGGTCACCGAGTGTGATAGTGCATATGATTAAT 1521	
QY	99	AlaAspLys-----AlaLeuValHisGlnPheGlnProHisLys 111	
DB	1522	TATGACAAAGATAATCAAAACAGGGTTGTAGCGACTACCCCTCTGTGAAAAATAATAA 1581	
QY	112	GlyTyr-----GlyTyrPhe 116	
DB	1582	GGTGTGTGGCAGCAGTACTTGATCTATAATAGGTATTAAAAACTATATCTGGTTACTAT 1641	
QY	117	-----AspTyrGlyLysAspIleAsnTrpGlnMetTrpProValLysAsp 131	
DB	1642	TATCTTTACGAATAAAACAGAGTAGGATAAGTTAAGATTTAGATCTCTATGCAAG 1701	
QY	132	AsnGluValArgTrpGlnLeuHisArgVal-----LysTrpTrpGlnAlaMet 147	
DB	1702	TCATTAGCAGTGGGAGTAGTAAATCTGTTAATGACGATATAAAACGGCTAAAGCAGCT 1761	
QY	147	----- 147	
DB	1762	TTTGTAATCAAGTCAACTGGACCTAAATAATTTAAGTTTCTGCTAAAAATGCTAATTTT 1821	
QY	148	-----AlaLeuValTyrHisAlaThrGlyAspGluLysTyrAlaArgGlu 162	
DB	1822	AAAGGAAAACAGATCTGTATATAC-----GAAGCACATGTAAAGAC 1866	
QY	163	TrpValTyrGlnTyrSer---AspTrpAlaArgLysAsnProLeuGly---LeuSerGln 180	
DB	1867	TTCACTTCTGATCAATCTTTGGACGGGAAATTAATAAAATCAACTTGTACCTTTGCAGCC 1926	
QY	181	AspAsnAspLysPheValTrpArgProLeuGluValSerAspArgValGlnSerLeuPro 200	
DB	1927	TTTTTCAGAAACTAGATATTACAAATTAGGAGTTACACAACTCAGCTTTTACCG 1986	
QY	201	ProThrPheSerLeuPheValAsn-----SerProAlaPheThrPro 214	
DB	1987	GTATTGAGTTATTTTATGTTAATGAATGGAATAAGTCAGCTCAACAGCTTACACTTCC 2046	
QY	214	----- 214	
DB	2047	TCAGACAATPATATAATTTGGGCTATGACCCACAGAGCTATTTTGCTCTTTCTGGAATG 2106	
QY	215	-----AlaPheLeuMetGluPheLeuAsn 222	
DB	2107	TATTCAGAGAAACCAAGATCCATCAGCAGCTATCGCCGAATTAACAAATTAATACAT 2166	
QY	223	SerTyrHisGlnGlnAla-----AspTyrLeuSerThrHisTyrAlaGlu 237	
DB	2167	GATATTCAATAACGTGGCATGGGGTTATACTTTGTATGCTCTATAATCACACTGCAAAA 2226	
QY	238	GlnGlyAsnHisArgLeuPheGlu---AlaGlnArgAsnLeuPheAlaGlyValSerPhe 256	
DB	3118	GCA-----GGTTTAATACATTAAAGCGGTTCAACAGATGCTTTCCGGAAATTGAGC 3168	
DB	2227	ACT-----TATCTCTTTGAGGATATAGAACTAATTTATTAT-----CACTTT 2268	
QY	257	ProGluPheLysAspSerProArgTrpArgGlnThrGly----- 269	
DB	2269	ATGAATGAAGATGGTTTCAACCAAGAGAAAGTTTGGAGGGGAGCGTTTAGGAACCACTCAT 2328	
QY	270	-----IleSerValLeuAsnThrGluLysLys 279	
DB	2329	GCAATGAGTCGTCGTGTTTGGTTGGATTCTCAATAATATCTTCAAGTGAATTTAA----- 2385	
QY	280	GlnValTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHisValAlaAlaIle 299	
DB	2386	-----GTTGATGGTTTCCGTTTGTATGATCATGGAGATCATGATGGCTGGCAT 2436	
QY	300	AspIlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeuGluLysGluPhePro 319	
DB	2437	GAATTA-----GCTTATAAAGAGCTAAAGCTAATTAAT----- 2469	
QY	320	GlnSerTyrValGlnThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuPro 339	
DB	2470	-----CCTAATATGATT----- 2481	
QY	340	AspTyrAsnThrProMetPheGlyAspSerTrpIleThrAspLysAsnPheArgMetAla 359	
DB	2482	-----ATGATTGGTGAGGGCTGG-----AGAACAATC 2508	
QY	360	GlnPheAlaSerTrpAlaArgValPheProAlaAsnGln----- 372	
DB	2509	CAAGGCGATCAAGGTAAAGCCGTTAAACCCAGCTGACCAAGATTGGATGAAGTCAACCGAT 2568	
QY	373	AlaIleLysTyrPheAlaThrAspGlyLysGlnGlyLysAlaProAsnPheLeuSerLys 392	
DB	2569	ACAGTTGGCGCTCTTTCAGATGATTCGT-----AATAGCTGAATCT 2613	
QY	393	AlaLeuSerAsnAlaGlyPheTyrThrPheArgSerGlyTrpAspLysAsnAlaThrVal 412	
DB	2614	GGTTTTCCAAATGAAGTACTCCAGCTTTCATCACAGGTGGCCCACAATTTTACAAGGT 2673	
QY	413	MetVal-----LeuLysAlaSerPro-----ProGly----- 421	
DB	2674	ATTTTAAATAATCAAGCAACCACTGGGAATTTTGAACGAGATTCGCCAGAGATGTG 2733	
QY	422	---GluPheHisAlaGlnProAspAsnGlyThrPhe---GluLeuPheIleLysGlyArg 439	
DB	2734	GTGCACTATATTGCTCCACATGATACCTTACCTTCGATCATGTGATGCATAATCAATT 2793	
QY	440	AsnPheThrProAspAlaGlyValPheValTyrSerGlyAspGluAlaIleMetLysLeu 459	
DB	2794	AATAAAGACCTTAAGTA-----GCTCAAGAGATATT----- 2826	
QY	460	ArgAsnTrpTyrArgGlnThrArgIleHisSerThrLeuThrLeuAspAsnGlnAsnMet 479	
DB	2827	-----CATGACGCTGCTGTTTAGGAATGTATGATTTTAACTCTCAAGGACA 2877	
QY	480	ValIleThrLysAlaArgGlnAsnLysTrpGluThrGlyAsnAsnLeuAspValLeuThr 499	
DB	2878	GCATTCATTTCATTCGTCAAGATGATGTCGTACGAAGCGTTTACTTAACCTGATTAC 2937	
QY	500	TyrThrAsnProSerTyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsnLys 519	
DB	2938	ATGACAAAAAGTTTCAGATGACAAAATTCCTTAATAAAGCAACACTTATTGAAGCTGTA 2997	
QY	520	LysTyrPheLeuValIleAspArgAlaIleGlyGluAlaThrGlyAsnLeuGlyValHis 539	
DB	2998	GAATACCCATATTTTATTCATGATCATATGATCTTCAGATGCCATTAATCATTTTGT 3057	
QY	540	TrpGlnLeuLysGluAspSerAsnProValPheAspLysThrLysAsnArgValTyrThr 559	
DB	3058	TGGGAGCAGCCACAGATAATAACAAACACCAAAATTTCAACGAAAAACACAGGCTATACA 3117	
QY	560	ThrTyrArgAspGlyAsnAsnLeuMetIleGlnSerLeuAsnAla-----Asp 575	
DB	3118	GCA-----GGTTTAATACATTAAAGCGGTTCAACAGATGCTTTCCGGAAATTGAGC 3168	

Qy		576	ArgThrSerLeuAenGluGluGlyValSerTyrValTyrAsnLysGluLeuLys	595
	:::	:		:::::
Db		3169	AAGCAGAATAATGCATCGTAGGTTCATTACAGAGGTAGCTCAAGGTGATATTAAA	3228
	:	:		:::::
Qy		596	ArgProAlaPheValPheGluLysProLysIysAsnAlaGlyThrGlnAenPheValSer	615
	:	:		:::::
Db		3229	GAAAGAGATTGGTTATT-----GCTTACCACAATAGATTCTAAAGCGCATATTTC	3282
	:	:		:::::
Qy		616	IleValTyrProTyrAspGlyGlnLysAlaProGluLeuSerIleArgGlu-AsnLysGI	635
	:::	:		:::::
Db		3283	GCAGTATTTGTTAATGCTGATAGTAAAGCTAGAAACGTTTTACTAGGTGAATAATA--	3340
	:	:		:::::
Qy		635	YAsnAspPheGluLysGlyIlysLeuAenLeuThrLysIleasnGlyLysGlnGlnLe	655
	:	:		:::::
Db		3341	-AACACCTTTTAAAGGCCAAGTAATTGTTGATCTGATCAAGCGGGATTAAACCAATC	3399
	:	:		:::::
Qy		655	uValLeuVal	658
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Db		3400	TCAACTCCTA	3409

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RESULT 10
US-10-320-797-2302
; Sequence 2302, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2302
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1666)..(1666)
; OTHER INFORMATION: n=g, a, t or c
US-10-320-797-2302

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Alignment Scores:	
Pred. No.:	0.0061
Score:	121.00
Percent Similarity:	36.55%
Best Local Similarity:	20.52%
Query Match:	3.46%
DB:	16
	Length: 2541
	Matches: 151
	Conservative: 118
	Mismatches: 252
	Indels: 222
	Gaps: 37
US-09-802-285A-2 (1-659) x US-10-320-797-2302 (1-2541)	

Qy	8	ArgIleIleValPheAlaValIleAlaLeuSerGlyAsnIleLeuAlaGlnSer	27
Db	106	AGGGTGTCTGTCTTTGACTTGGTGAAACAACAGTCGAAGCACATTCGCCCTTTGAGAAC---	162
Qy	28	SerIleThrArgLysAspPheAspHisIleAsnLeuGluTy-SerGlyLeuGluLysVal	47
Db	163	-----AGAAAATAATCCGCTCAATTGCCTCTTCTCCAGATGCG-----	201
Qy	48	AsnLysAlaValAlaAlaGlyAsnTrpAspAlaAlaLysAlaLeuAlaTrpYr	67
Db	202	AATGTACTAATT-----TCCATCGACGAAGATGGAAGACACTGTTGTGCACCTC	252
Qy	68	ArgGluLysSerLysAlaArgGluProAspPheSerAsnAlaGluLysProXlaAspIle	87
Db	253	CGTAAGGGGACA-----	264

Qy	88	ArgGlnProIleAspLysValThrArgGluMetAlaAspLysAlaLeuValHis	105
Db	265	-----GTTTTCACCACTCTCTTCAAGCGCAAGTCCACACGTT	306
Qy	106	GlnPheGlnProHisLysGlyTyrGlyTyrPheAspTyrGlyLysAspIleAsnTrpGln	125
Db	307	TCATTTTCTCCGAGCGCAATATATTGCATTAACGCACGGTCAATGGTG	360
Qy	126	MetTrpProValLysAspAsnGluValArg	140
Db	361	ATATGGAACTCCACCCATTTGGTCCGAGAGTTTGCACCTTTTACCTCCATAGGAG	420
Qy	141	-----ValLysTrpTrpGlnAlaMetAlaLeuVal	150
Db	421	TATACTGGTCATCACGACGAAGTTGTAGTGTCTGCTGGTC-CAAAACCTCCAGGTATT	479
Qy	151	TyrHisAlaThrGlyAspGluLysTyrAlaArgGlnTrpValTyrGln	166
Db	480	TATCACTACCTC-----GAGAGATATGCTGGAGGCTATATACCAATTAACTCCACTTGA	533
Qy	167	-----Tyr	167
Db	534	AGGTTTCCAACTAAGCAATTGGGGACATAGAGATGTTGTGGAGCGTCTTTTC	593
Qy	168	Ser-AspTrpAlaArgLysAsnProLeuGlyLeuSerGlnAspAsnAspLysPheValTr	187
Db	594	TCAAGT-----GAGAAGACTATTATACCGGTTTCTCGAGACGGTCAGTGTGTGATG	647
Qy	187	PAIqProLeuGlu--ValSerAsp-ArgValGlnSerLeuProProThrPheSerLeuP	206
Db	648	GAAGCAAAAGAGGCGTCTCTGAGCGGACTCCGATGTTGAGATGACATTTCTGAATC	707
Qy	206	heValAsnSerProAlaPheThrProAlaPheLeuMetGluPheLeuAsnSerTyrHisG	226
Db	708	TCCACCACTTCCACCTCTCGGCCAACCTTGCC-CTTGAGACCGCGCTCGCTAC	762
Qy	226	lnGlnAlaAspTyrLeuSerThrHisTyrAlaGlnGlnGlyAsnHisArgLeuPheGluA	246
Db	763	-----ACTCGATGGGGGTTTCACTCGCTCGCACTT-CTT	794
Qy	246	laGlnArgAsnLeuPheAlaGlyValSerProGluPheLysAspSerProArgTrpA	266
Db	795	-----CAACCAACCTGGT	807
Qy	266	rgGlnThrGlyIleSerValLeuAsnThrGluIleLysLysGlnValTyrAlaAspGlyM	286
Db	808	ACGAAGTGATTGGCTACTCTCCACCCAA	839
Qy	286	etGlnPheGluLeuSerProIleTyrHisValAlaAlaIleAspIlePheLeuLysAlaT	306
Db	840	-----AACATCTCTCT	885
Qy	306	yrGlySerAlaLysArgValAsnLeuLulysGluPheProGlnSerTyrValGlnThrV	326
Db	886	TGGAGATGCC-----CGAATTTACCCCGTACATCGTTG--TCGA	925
Qy	326	alGluAsnMetIleMetAlaLeuIleSerLeuProAspTyrAsnThrProMetP	346
Db	926	TCTCCAACGAGAGATCTCTAGTGTGGCAGTCTCCGG	963
Qy	346	heGlyAspSerTrpIleThrAspLysAsnPheArgMetAlaGlnPheAlaSerTrp	364
Db	964	--TCGGAGAGTGGTTGGCATTTGGGCGCGCAAGCTCGCAGAGTATTGTTGGGAAT	1021
Qy	365	-----AlaArgValPheProAlaAsnGlnAlaIleLysTyrPhe	377
Db	1022	GGCAGAGTGAGAGTTACGTTCTTAAACAGCAAGGCTCACTACTACGACATGAACACCTCG	1081
Qy	378	-----AlaThrAspGlyLysGlnGlyLysAlaProAsnP	389
Db	1082	CGTTTACTCCGATGGGCAGAACTACTCTACTGGCGGTGAAGTGGTAAGTCAAG	1137
Qy	389	heLeuSerLysAlaLeuSerAsnAlaGlyPheTyrThrPheArgSerGlyTyrAspLysA	409


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Db 1138 --TTATGGAATGCTTCAAGTGGCTTCGCTTTGTGACCTTCCT-----GAACACA 1186
QY snalathrvalmetvalleuLysAlaSerProProGlyGlu-----PheHisAlaGlnP 427
Db 1187 CTGCGGTATCTCCACTGTGCAATTTGCTAAGCAGGACAACTTTTATTACACAGCGTCC 1246
QY 427 roAspaanglythrPheGluLeuPhe-----lleLysGlyArgAsnPhetheThrProAspA 445
Db 1247 TTGAC---GGTACTGTCCGCGCATACGACCTCATCCGATCCGTAACCTTC----- 1293
QY 445 laGlyValPheValTyrSerGlyAspGluAlaIleMetLysLeuArgAsnTyrPyrArgG 465
Db 1294 -----CGGACATTCACCTCTC 1309
QY 465 lnThrArgIleHis---SerThrLeuThrLeuAspAsnGlnAsnMetValIleThrLysA 484
Db 1310 CCACCCCTGCTCCAGTCTCTGCGCTCGCGCTCGATCCTCAGGCGATGTGCTGTGCTG 1369
QY 484 laArgGlnAsnLysTrpGlu-----ThrGlyAsnAsnLeuAspV 497
Db 1370 GATCTCAAGATTCCTTCGAGATCTACATGTGTCAGTCCAAACCGGTAAACTGCTTGACA 1429
QY 497 alLeuThr---TyrThrAsnPro---SerTyrProAsn---LeuAspHisGlnArgSerV 514
Db 1430 TCTCTACTGCCATACCGCTCTCTATATACAG-CCTCGCTCTCTCTCCACCGGTAACTCAG 1488
QY 514 al---LeuPheIleAsnLysLysTyrPheLeuValIleAspArgAlaIleGlyGluAlar 533
Db 1489 TTGGCATCTCTCTCTGGGATCGTTCATCC-GTT-----TATGGTCAGTCTT 1535
QY 533 hrGlyAsnLeuGlyValHisTrpGlnLeuLysGluAspSerAsnProValPheAspLysT 553
Db 1536 CGGCGCAT-----CAAGACCCACCGAACCAGTTCAGCTTCCTGGG 1574
QY 553 hrLysAsnArgValTyrThrTyrArgAspGlyAsnAsnLeuMetIleGlnSerLeuA 573
Db 1575 CGAAGCGACTCGCTTGGCGTTCAGG-CCTGACCGAATGAGATCTGCGCTTCTACTTTGA 1633
QY 573 snalalaspArgThrSerLeuAsnGluGluGluLysValSerTyrValTyr-----A 591
Db 1634 ACGGGAATTTGATCTTTATCGATGTGGAAGAANGACAGATTAACTCTGTATTATTAAGGCC 1693
QY 591 snLysGlnLeuLysArgProAlaPheValPheGluLys-----ProLysLysAsnAlaG 609
Db 1694 GAAGAGATATTTCTGGAGGAGAAAGTGATGATCAGCGCTTACAGCTGCCAATAACCCCG 1753
QY 609 lyThrGlnAsnPheValSerIleValTyrProTyrAsp-----G 622
Db 1754 CAAGCAAGTATTTCAACAGTGTCTATCTACACTGCCGACGGTGTGTGTCTTGGCTGGTG 1813
QY 622 lyGlnLysAlaProGluIleSerIleArgGluAsnLysGlyAsnAspPheGluLysGlyL 642
Db 1814 GAAGACGACAAAGTATGTTGTGTGTPATGATCGGACGGAAGCGGTGATGCTGAAGAAGTTC 1873
QY 642 ysLeuAsnLeuThrLeuThrIleAsnGlyLysGlnGlnLeuVal 656
Db 1874 AGATCAGCAAAATCTCAGCTTGGACGGTACGCAAGAGATGTTG 1917
```

RESULT 11

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US-10-369-493-46899
; Sequence 46899, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
```

```
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46899
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Bacillus subtilis
; US-10-369-493-46899

Alignment Scores:
Pred. No.: 0.00559 Length: 2034
Score: 120.00 Matches: 126
Percent Similarity: 32.77% Conservative: 87
Best Local Similarity: 19.38% Mismatches: 214
Query Match: 3.43% Indels: 224
DB: 16 Gaps: 32

US-09-802-285A-2 (1-659) x US-10-369-493-46899 (1-2034)
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QY 41 TyrSerGlyLeuGluLysValAsnLysAlaValAlaAlaGlyAsnTyrAspAspAlaA 60
Db 313 TTTTCTGGAAGCGCAGTTGTAGATAAAATAACACAGCGGTTTCAACAGGCAAGAG 372
QY 61 LysAlaLeuLeuAlaTyrTyr-----ArgGluLysSerLysAlaArgGluProAsp 77
Db 373 AAGCGCTTGTGCGCATTTATACAGGATCGGGAAGGCCATCAAGTGCMAAGTATTGCC 432
QY 78 PheSerAsnAlaGluLysProAlaAspIleArgGlnProIleAspLysValThrArgGlu 97
Db 433 TATAGCAACACACAAA-----GGAAGAACATGGACGACGAG 465
QY 98 MetAlaAspLysAlaLeuValHisGlnPheGlnProHisLysGlyTyrGlyTyrPheAsp 117
Db 466 TAGCGTGGCAACCTCTGTCAAT-----CCAAACCCGGT 498
QY 118 TyrGlyLysAspIleAsnTrpGlnMetTrpProValLysAspAsnGluValArgTyrGln 137
Db 499 ---AAAAAGATTTT-----CGCGATCCAAAGTCTTTGGTAT 534
QY 138 LeuHisArgValLysTrpTrpGlnAlaMetAla-----LeuValTyrHis 152
Db 535 GAGAAAGAAAAAAGTGGGTGATGCTTTCGCGCGCGTGCACCGAATCCTCATTTAT 591
QY 153 AlaThrGlyAspGluLysTyrAlaArgGluTrpValTyrGlnTyrSerAspTrpAlaArg 172
Db 592 -----ACATCAAAAAATCTGAAGCAGTGGACGTAT 621
QY 173 LysAsnProLeuGlyLeuSerGlnAspAsnAspLysPheValTrpArgProLeuGluVal 192
Db 622 GCAAGTCAATTTGGACAGGATCAAGNAGCCACGGGGAGTATGG----- 666
QY 193 SerAspArgValGlnSerLeuProProThrPheSerLeuPheValAsnSerProAlaPhe 212
Db 667 -----GAAATGCCGGATTTATTATTGAGCTTCCGCTAGACGCGCAATCCGAAT 711
QY 213 ThrProAlaPheLeuMetGluPhe-----LeuAsn 222
Db 712 CAAAGAAATGGGTCAATGCGAGTCAGTTCGGAACCGAGCGGTCTCGGAGGATCAGGC 771
QY 223 SerTyrHisGlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGly-----Asn 240
Db 772 ATGCAATATTTTGTAGGGGACTTTGATGGAACATCAITTTAAAAATGAAACCCGCCAAC 831
QY 241 HisArgLeuPhe---GluAlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPhe 259
Db 832 AAAATTCTCTGGACGGATTAACGCGAGAGACTTTTATCGGCTGTATCTCGTCTGATATT 891
QY 260 -----LysAspSerProArg----- 264
Db 892 CCATCCACAGACAGCCCGCGCTATGTTAGGTGGATGAGCAATTGGCAATATGCGAAT 951
QY 265 -----TrpArgGlnThrGlyLeuSerValLeuAsnThrGluIleLys 276
```


Db	952	GATGTTCCGACATCCCATGGAGAGTGCA-----ACGTCCATTCCAAGAGTAAAA	1005	Db	1935	TGTGATTGATGCACATGATTCCGTATTTCAGAGGCCCAATTGGCTTGAATGTGTGG--	1992
Qy	279	LysGlnValTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHisValAlaAla	298	Qy	541	nLeuLysGluAspSerAsnProValPhe	550
Db	1006	TTGAAGCGTTTACCGAAGGGTTAGAGTGGTCCAAACACCGGTGAAGAGCTGGAACC	1065	Db	1993	-----GACGGCACTGCTGTCTTT	2010
Qy	299	Ile-----AspIle	301	RESULT 12			
Db	1066	ATTCCGGGAACCTTAAGAAGTGAAGATCTGCACATATCCCTCGCAAGTCATATGTG	1125	US-10-369-493-26002			
Qy	302	PheLeuLysAlaTyrGlySerAlaLysArgValAsnLeuGlu---LysGluPheProGln	320	; Sequence 26002, Application US/10369493			
Db	1126	TTAGCGGGCAATCGAGATCCCTATGAATAAATATGCAATTTAAAGTAAGCCCTGGT	1185	; Publication No. US20030233675A1			
Qy	321	Ser-----TyrValGlnThrValGluAsnMetIleMet-----	331	; GENERAL INFORMATION:			
Db	1186	TCAGCTGCTGATTTGGTTTAAAGTCCGAACAGGTGAAATCAATTTACGAAGTCGCG	1245	; APPLICANT: Cao, Yongwei			
Qy	332	-----AlaLeuIleSerLeuSerLeuProAspTyrAsnThrProMetPhe	346	; APPLICANT: Hinkle, Gregory J.			
Db	1246	TATGACCGAAGAACGCCAAATTTGCTTGACCGAGCGAGTCAAGCAACGACACCTTT	1305	; APPLICANT: Slater, Steven C.			
Qy	347	GlyAspSerTrpIleThrAspLysAsn-----PheArgMetAlaGlnPheAlaSer	363	; APPLICANT: Goldman, Barry S.			
Db	1306	AATCGCGCTTTAAACACCGGAAAGAAACAGACCCCTTGAACCGGTAAATGGGAAGTT	1365	; APPLICANT: Chen, Xianfeng			
Qy	364	TrpAlaArgValPheProAlaAsnGlnAlaIleLysTyrPheAlaThrAspGlyLysGln	383	; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF			
Db	1366	AAGTTGCGCATTTTGTGACCGCTCCTCGGTGAAGTATTTGGGAATGACGGAAGCAG	1425	; FILE REFERENCE: 38-10(52052)B			
Qy	384	GlyLysAla-----ProAsnPheLeuSerLysAlaLeu-----Ser	395	; CURRENT APPLICATION NUMBER: US/10/369,493			
Db	1426	GTCATAACGGATATTATTCTCCACGACGATCAAGCAAAAGGCTTGAATATATGCTGA	1485	; CURRENT FILING DATE: 2003-02-28			
Qy	396	AsnAlaGly-----	398	; PRIOR APPLICATION NUMBER: US 60/360,039			
Db	1486	AATGGCGGTGAAGGTAAATCTTTACGATACACCCCTTTAAAAAGTATGGGGAACG	1545	; PRIOR FILING DATE: 2002-02-21			
Qy	399	-----PheTyrThrPheArgSerGlyTrpAspLysAsnAlaThrValMetValLeuLys	416	; NUMBER OF SEQ ID NOS: 47374			
Db	1546	ACACCTTTATCTCCAATATGACTGGCTG-----ACGACTGA-----	1584	; SEQ ID NO 26002			
Qy	417	AlaSerProProGlyGluPheHisAlaGlnProAspAsnGlyThrPheGluLeuPheIle	436	; LENGTH: 1737			
Db	1585	-----AATGGACCGTGGCAGACACAAT	1608	; TYPE: DNA			
Qy	437	LysGlyArgAsnPheThrProAspAlaGlyValPheValTyr-----SerGlyAsp	453	; ORGANISM: Schizosaccharomyces pombe			
Db	1609	GAGGGAACACAGGAGGTGCGACGGCGATTCTTTATCTTCTCTTCAGCATCCGGGTCA	1668	US-10-369-493-26002			
Qy	454	Glu-AlaIleMetLysLeuArgAsnTrpTyrArgGln-----	465	Alignment Scores:			
Db	1669	GACTTCACTATGATCATCATCAATTAAGATGGAACCGAAGAGGGGCGAGGCA	1728	Pred. No.: 0.00649			
Qy	466	-----ThrArgIleHisSerThrLeuThrLeuAspAsnGlnAsnMetVa	480	Score: 118.50			
Db	1729	CTAATGTTTCGCTCTGACAAAGATGCCAAAACGGTTACCTTGCC-AAATGTGGATCGGAA	1787	Percent Similarity: 34.96%			
Qy	480	IleThrLysAlaArgGlnAsnLysTrpGluThrGlyAsnAsnLeuAspValLeuThrTy	500	Best Local Similarity: 20.86%			
Db	1788	GCATGACCTAGTGAATCTTTAAATTTGAGAACGGTGTGCTTCTGTCTATCTGCTGAATA	1847	Query Match: 3.39%			
Qy	500	rThrAsnProSerTyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsnLysTy	520	DB: 16			
Db	1848	CAAAACACCG-----ATAGACGCTTAATAAAAAA	1874	US-09-802-285A-2 (1-659) x US-10-369-493-26002 (1-1737)			
Qy	520	STYrPheLeu-----ValIleAspArgAl	528	Qy 112 GlyTyrGlyTyrPheAspTyrGlyLysAspIleAsnTrpGlnMetTrpProValLysAsp			131
Db	1875	GATCATCTGAAACACAGAGCGCGATCGCTTTAAATCTATTTAGATGATCGTCT	1934	Db 208 GGTATGATGTTCTTGATTAC---AAACAATGACTCTCGATATGAAGACTTTAGAGAT			264
Qy	528	atIleGlyGluAla-----ThrGlyAsnLeuGlyValHis---TrpGlu	541	Qy 132 ---AsnGluValArgTrpGlnLeuHisArgValLysTrpTrpGlnAlaMetAlaLeuVal			150
				Db 265 TTGGACAGCTTAATGAAAGCTCTACAGAAAGGACATGAAGTTAGTTATGACTTGTGTG			324
				Qy 151 TyrHisAlaThrGlyAspGluLysTyrAlaArgGluTrpValTyrGlnTyrSerAspTrp			170
				Db 325 TTAAACCACTCTTGATCAA-----CATGAGTGG---TTTAAGAGTCCAGATCT			372
				Qy 171 AlaArgLysAsnProLeuGlyLeuSerGlnAspAsnAspLysPheValTrpArgProLeu			190
				Db 373 TCTAAACAATAATCCG-----AAGCGAGATTGGTACTTTTGGAAACCCAGCT			417
				Qy 191 GluValSerAspArgValGlnSerLeuProProThrPheSerLeuPheValAsnSerPro			210
				Db 418 AGGTACAATGAAAAAGGCGACGCTTACCCCA-----			450
				Qy 211 AlaPheThrProAlaPheLeuMetGluPheLeuAsnSerTyrHisGlnGlnAlaAspTyr			230
				Db 451 -----AATAATGGAGAGCTATTTCGACTACT			477
				Qy 231 LeuSerThrHisTyrAlaGluGlnGlyAsnHisArgLeuPheGluAlaGlnArgAsnLeu			250
				Db 478 TCGGCGTGGGAATGGACGACGACTACGCAA-----GAATACTACCTACATCTT			525
				Qy 251 PheAlaGlyValSerPheProGluPheLys---AspSerProArgTrpArgGlnThrGly			269
				Db 526 TGGTCC--GTAGGCAACCCCGATCTTAATTTGGGAAACCCCAAAAGTTAGGGAACGGGTA			582
				Qy 270 IleSerValLeuAsnThrGluIleLysLysGlnValTyrAlaAspGlyMetGlnPheGlu			289

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Db 583 CACGATATCTACGTTCTGCTGTAGAGAGTA-----GATGG-----TTTCGA 630
Qy 290 LeuSerProIleTyrHisValAlaAlaIleAspIlePheLeuLysAla----- 305
Db 631 CTTGATGCTATTAAACATGATCAGCAAGAGTTCTTAGATGCTCCAAATTAAGTAT 690
Qy 306 -----TyrGlySerAlaLysArgValAsnLeu 314
Db 691 GACAGGTACGAATATCAACTAGCCTATCAATATPACGCCAATGTCGCCAATTCAC-- 747
Qy 315 GluLysGluPheProGlnSerTyrValGlnThrValGluAsnMetIleMetAlaLeuIle 334
Db 748 -----GAGTATCTAATGGGATAGCAATAT----- 774
Qy 335 SerIleSerLeuProAspTyrAsnThrProMetPheGlyAsp---SerTrpIleThrAsp 353
Db 775 -----CTTACAGAGTATGACGCTTTTCTGTAGGGAAATGCCCTTACGTTTTCGAT 825
Qy 354 LysAsn-----PheArgMetAlaGln 360
Db 826 ACGACGAATCTGCATGCTGTGTGCTGATCGTAGAAGTACGATGATATTCAG 885
Qy 361 PheAlaSerTrpAlaArgValPheProAlaAsnGlnAlaIleLysTyrPheAlaThrAsp 380
Db 886 TTTGATTTTGTGACCTTGATCTCGATCCTTAATCAGCAT---AAGTATATTTGAAGAGT 942
Qy 381 GlyLysGlnGlyLysAlaProAsnPheLeuSerLys-----AlaLeuSerAsn 396
Db 943 TGGGAGCTTCTCTGATTTGAAAGATCTTAAAGAAATGGCAGTCTGCACTACTTTTCGGT 1002
Qy 397 AlaGlyPhe---TyrThrPheArgSerGlyTyrAspLysAsnAlaThrVal---MetVal 414
Db 1003 GTGGTGTGAATGCTCTTATTGTAAATCACCACCAACGAGAACTGTTTCACGATAT 1062
Qy 415 LeuLysAlaSerProProGlyGluPheHisAlaGlnProAspAsnGlyThrPheGluLeu 434
Db 1063 CTTTCTGATCTCCCAAGTAGACATATAGCTCCAAATTTGATGGCTCTTTTATCATA 1122
Qy 435 PheIleLysGlyArgAsnPheThrProAspAlaGlyValPheValTyrSerGlyAspGlu 454
Db 1123 TTCCAAGTGGT-----ACCCCA-----TTGTATTCCAGGTCAGAA 1161
Qy 455 AlaIleMetLysLeuArgAsnTyrTyrArgGlnThrArgIleHisSerThrLeuThrLeu 474
Db 1162 -----CTTGCTCTTGCCAAATATCCACGAGATGGCCGATGATGATACCTTGATGTT 1215
Qy 475 AspAsnGlnAsnMetValIleThrLysAlaArgGlnAsnLysTrpGluThrGlyAsnAsn 494
Db 1216 GAAACGCAGAACTTC-----TGGA----- 1236
Qy 495 LeuAspValLeuThrTyrThrAsnProSerTyrProAsnLeuAspHisGlnArgSerVal 514
Db 1237 -----CTTTTATGATGGCAATCTCTAGTCAGAGAAAT-----GAGAAGACTATG 1284
Qy 515 LeuPheIleAsnLysLysTyrPheLeuValIleAspArgAlaIleGlyGluAlaThrGly 534
Db 1285 GACATTGTTACAAACGT-----GCTCGTGACACGGT 1317
Qy 535 AsnLeuGlyValHisTrpGlnLeuLysGluAspSerAsnProValPheAspLysThrLys 554
Db 1318 CGCACACCAATGATTTGG-----GATAGCTCACCAACGGTGTTCACAAAG 1365
Qy 555 -----AsnArgValTyrThrThrTyrArgAspGlyAsnAsnLeuMet 568
Db 1366 GTGGAGTAAACCGGTGATGAGAGTGACTAATGACTACAAAGATGGAAT----- 1416
Qy 569 IleGlnSerLeuAsnAlaAspArgThrSerLeuAsnGluGluGlyLysValSerTyr 588
Db 1417 -----GCTGCCAATCAAGTTAATGACCTGAAAGTCTTACACATT 1458
Qy 589 -----ValTyrAsnLysGluLeuLys 595
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Db 1459 TGGTCAAGGCATTGGAGCTTCGTAAAGAATTGAAG 1494
RESULT 13
US-10-369-493-26008
; Sequence 26008, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 39-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 26008
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-26008
Alignment Scores:
Pred. No.: 0.00649 Length: 1737
Score: 118.50 Matches: 111
Percent Similarity: 34.96% Conservative: 75
Best Local Similarity: 20.86% Mismatches: 195
Query Match: 3.39% Indels: 151
DB: 16 Gaps: 31
US-09-802-285A-2 (1-659) x US-10-369-493-26008 (1-1737)
Qy 112 GlyTyrGlyTyrPheAspTyrGlyLysAspIleAsnTrpGlnMetTrpProValLysAsp 131
Db 208 GGTATGATGTTTCTGATTAC---AAACAATTGACTCTCGATATGGAATTTAGAGAT 264
Qy 132 ---AsnGluValArgTrpGlnLeuHisArgValLysTrpTrpGlnAlaMetAlaLeuVal 150
Db 265 TTGCACAGGCTAATAAGAGCTCTACACGAAAGGACATGAAGTAGTTATGGACTTGGTG 324
Qy 151 TyrHisAlaThrGlyAspGluLysTyrAlaArgGluTrpValTyrGlnTyrSerAspTrp 170
Db 325 TTAACCCACACTTCTGATCAA-----CATGAGTGG---TTTAGAGGAGTCCAGATCT 372
Qy 171 AlaArgLysAsnProLeuGlyLeuSerGlnAspAsnAspLysPheValTrpArgProLeu 190
Db 373 TCTAAACAATCCG-----AAGCGAGATTGGTACTTTTGGAAACCAAGCT 417
Qy 191 GluValSerAspArgValGlnSerLeuProProThrPheSerLeuPheValAsnSerPro 210
Db 418 AGGTACAATGAAAGGCGAAGCGCTTACCCCA----- 450
Qy 211 AlaPheThrProAlaPheLeuMetGluPheLeuAsnSerTyrHisGlnGlnAlaAspTyr 230
Db 451 -----ATAATTTGGAGAAAGCTATTTCGATACT 477
Qy 231 LeuSerThrHisTyrAlaGluGlnGlyAsnHisArgLeuPheGluAlaGlnArgAsnLeu 250
Db 478 TCGCGCTGGGAATGGGACGAAGCTACGCA-----GAATACTACTACATCTT 525
Qy 251 PheAlaGlyValSerPhePheProGluPheLys---AspSerProArgTrpArgGlnThrGly 269
Db 526 TGTGTC---GTAGGGCAACCCGATCTTAATTGGGAAACCCCAAGTTAGGAAGCGGTA 582
Qy 270 IleSerValLeuAsnThrGluLysLysGlnValTyrAlaAspGlyMetGlnPheGlu 289
Db 583 CACGATATCTAGTTCTGCTGTAGAGAGTA-----GATGG-----TTTCGA 630
Qy 290 LeuSerProIleTyrHisValAlaAlaIleAspIlePheLeuLysAla----- 305
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Db 5278 TATCAAAAAATTTACGAAGAGTATGGAGATATGGCGACTTTTGATCAATTTACTTCAAGGT 5337
Qy 138 LeuHicArgVallylserTrpGlnAlaMetAlaLeuVallylserHisAlaThrGlyAspGlu 157
Db 5338 TTACACGACGCGCAAAATGAACACTTGTAAATGGATCTTGTCTTAAACCATACTCTCTGATGAA 5397
Qy 158 LysTyrAlaArgGluTrpValTyrGlnTyrSerAspTrpAlaArgLysAsnProLeuGly 177
Db 5398 -----CACAGTGG-----TTTGAGGAAATCCGAAAAATCCAAAGCAACCGGTAC--- 5442
Qy 178 LeuSerGlnAspAsnLysPheValTrpArgProLeuGluValSerAspArgValGln 197
Db 5443 -----AGAGATTACTATTCTCGCGCGAG-----GAAAAACGAAATCAAT 5481
Qy 198 SerLeuProProThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeu 217
Db 5482 AACTGGGGCTCGATTTTTCAGC-----GGTCCAGCATGGGAA-----TTG 5520
Qy 218 MetGluPheLeuAsnSerTyrHisGlnGlnAlaAspTyrLeuSerThrHisTyrAlaGlu 237
Db 5521 GACGAAAAACAGGTGAGTAC-----TATTTACACCTGTTCTCCAAAAA 5565
Qy 238 GlnGly-----AsnHisArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSer 255
Db 5566 CAACCTGATTTAAACTGGGAAACCCCTAAATTCGCCAAGATGTATATAATATGATGAAA 5625
Qy 256 PheProGluPheLysAspSerProArgTrpArgGlnThrGlyIle----- 270
Db 5626 TTC-----TGCTAGATAAAGCAVTTGATGGCTTCCCGCATG 5661
Qy 271 SerValLeuAsnThrGluIleLysLysGlnValTyrAlaAspGlyMetGlnPheGluLeu 290
Db 5662 GAGGTAAATTTTATTTCCAAAATACTGATTTCCAGATGTCCTCAGTACCAGAT--- 5718
Qy 291 SerProIleTyrHisValAlaAlaIleAspIlePheLeuLysAlaTyrGlySerAlaLys 310
Db 5719 GGTCAAAATTTTGGCGATGCTGGCAATGAT-----TTTTGTAATGGACCG 5763
Qy 311 ArgValAsnLeuGluLysGluPheProGlnSerTyrValGlnThrValGluAsnMetIle 330
Db 5764 CGGATTCAT-----GAGTCTTCGCAAGAAATGAACCAAGATTAATCTCTTAATATAC 5814
Qy 331 MetAlaLeuIleSerIleSerLeuProAspTyrAsnThrProMetPheGlyAspSerTrp 350
Db 5815 GATCTGATGACTGTGGCGAAATGCCCTGGCTAGTACA----- 5853
Qy 351 IleThrAspLysAsnPheArgMetAlaGlnPheAlaSerTrpAlaArgValPhe----- 368
Db 5854 ---ACCAC-----GCGCAAAATTTACACGAAT 5877
Qy 369 ProAlaAsnGlnAlaIleLysTyrPheAlaThr----- 379
Db 5878 CCAGCAAAATGAAGTCGATATGATTTTACATTTGAACATATGAACATAGATTCGAT 5937
Qy 380 ---AspGlyLysGlnGlyLysAlaProAsnPheLeuSerLysAlaLeuSerAsnAlaGly 398
Db 5938 GCGGACAAATAATGGGATCTAAAACCAATCTACTTACCAGATTTAAAAGAAAAATATGCT 5997
Qy 399 PheTyrThrPhe-----ArgSerGlyTrpAspLysAsnAlaThrValMetValLeu 415
Db 5998 GAATGGCAAGTCGCTTCAAGAAACGGTTGGAAAT----- 6033
Qy 416 LysAlaSerProProGlyGluPheHisAlaGlnPro----- 427
Db 6034 -----AGCTTATATGGAATATCATGACCAACCGGTATCGTTTCTCGTTTGGGAAT 6087
Qy 428 AspAsn-----GlyThrPheGluLeuPheIleLys 437
Db 6088 GACAAATCGTTTCCCGTGTTCGTTCCAGCAAAATGCTTGCACACTGTTTGCATATGATGAAA 6147
Qy 438 GlyArgAsnPheThrProAspAlaGlyValPheValTyrSerGlyAspGluAlaIleMet 457
Db 6148 GGA-----ACGCCA-----TATATTATCAAGTGAAGAAATTTGGGATG 6186
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Qy 458 LysLeuArgAsnTrpTyrArgGlnThrArgIleHisSerThrLeuThrLeuAspAsnGln 477
Db 6187 -----ACAAATGTTCAITTTTGA-----ACGCTAGATGATTAC 6219
Qy 478 -----AsnMet----- 479
Db 6220 CGTGATATCGAAACGCTTAACATGTACAAAGAGCGTAAGGAGCAGACACAGCATGAA 6279
Qy 480 -----ValIleThrLysAlaArgGlnAsn-----LysTrp 489
Db 6280 AGCATCATGTCAGTCGATTTTACACAAAAGCGCTGACAATCGAGAACGCCGTACCACTGG 6339
Qy 490 GluThrGlyAsnAsnLeuAspValLeuThrTyrThr-----AsnProSer 504
Db 6340 GATAATAGCGAGATGCTGGCTTCACACCGGACCGCTTGGCTTAAAGTCAACCCCGCG 6399
Qy 505 TyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsnLysLysTyrPhe----- 522
Db 6400 TATACAGAAATCAACAAACGAAGAGCGCTGAAAAACCCAGATTCATTTCTACTACTAC 6459
Qy 523 -----LeuValIleAspArgAlaIleGlyGlu-----AlaThrGlyAsnLeuGlyVal 538
Db 6460 CAAATCTTATTAAAGTTTACGAAAAACGACTGAATCATCAACTGGTAATATTATCGTTG 6519
Qy 539 HisTrpGlnLeuLysGluAspSerAsnProValPheAspLysThrLysAsnArgValTyr 558
Db 6520 -----TTATTAACCTAAAGATGAAGCGATTTTC-----GCATAT 6552
Qy 559 ThrThrTyrArgAspGlyAsnAsnLeuMetIleGlnSerLeuAsnAlaAspArgThrSer 578
Db 6553 GAACGCTACACAGAAATGAAAAATTAGTGGTT-----TTATGTAAT 6594
Qy 579 LeuAsnGluGluGluGlyLysValSer-----TyrValTyrAsnLysGluLeuLysArg 596
Db 6595 TTCACAGAAAGAACAAAGTATTCTTCATGAAAAACATTTTGAACGAAATCCAAAAAGGT 6654
Qy 597 ProAlaPheValPheGluLysProLysLysAsnAlaGlyThr---GlnAsnPheValSer 615
Db 6655 TCCGTGCTGTAAACATGTTCTTAATATATAGAGGAACCTTTACGACCTTACGAAGCA 6714
Qy 616 IleValTyr 618
Db 6715 ATCGTTTAT 6723

RESULT 15
US-10-335-977-4204
; Sequence 4204, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
```

ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: GTN-018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 4204:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4455 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Helicobacter pylori
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...4455
 SEQUENCE DESCRIPTION: SEQ ID NO: 4204:
 US-10-335-977-4204

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 Query Match: 3.36% Indels: 189
 DB: 13 Gaps: 29

US-09-802-285A-2 (1-659) x US-10-335-977-4204 (1-4455)

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 QY 160 AlaArgGluTrpValTyrGlnTyrSerAspTrpAlaArgLysAsnProLeuGlyLeuSer 179
 DB 2008 GGTAAAAAGGGGATTTCGCT-----CCCTATGGCTTGAT 2043
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 QY 200 ProProThrPheSerLeuPheValAsnSerProAlaPheThrProAla-----PheLeu 217
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: July 31, 2004, 15:20:31 ; Search time 138 Seconds
(without alignments)
2650.092 Million cell updates/sec

Title: US-09-802-285A-2

Perfect score: 3494

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682709 seqs, 277475446 residues					

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued Patents NA:*

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- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	166.5	4.8	1950	4	US-09-134-000C-1897
6	132.5	3.8	2097	4	US-09-134-001C-795
7	123.5	3.5	3414	1	US-07-973-320-1
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14	115.5	3.3	3414	1	US-07-973-320-3	Sequence 3, Appli
15	115.5	3.3	3504	1	US-08-620-717A-8	Sequence 8, Appli
16	115	3.3	2859	5	PCT-US96-05320A-637	Sequence 637, App
17	115	3.3	16535	4	US-08-961-527-74	Sequence 74, Appli
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21	114.5	3.3	3504	2	US-08-590-554A-5	Sequence 5, Appli
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23	114.5	3.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
24	114.5	3.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1

US-08-258-639A-3
; Sequence 3, Application US/08258639A

; Patent No. 5681733

; GENERAL INFORMATION:

; APPLICANT: Su, Hongsheng

; APPLICANT: Blain, Francoise

; APPLICANT: Bennett, Clark

; APPLICANT: Gu, Kangfu

; APPLICANT: Zimmermann, Joseph

; APPLICANT: Musil, Roy

; TITLE OF INVENTION: Nucleic Acid Sequences And Expression

; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From

; TITLE OF INVENTION: Flavobacterium heparinum

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; STREET: 1455 Pennsylvania Avenue, N.W.

; CITY: Washington, D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/258,639A

; FILING DATE: 10 JUNE 1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Healey, William J.

; REGISTRATION NUMBER: 36,160

; REFERENCE/DOCKET NUMBER: 104385.116

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)942-8400

; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-258-639A-3

Alignment Scores:

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Score: 3494.00 Matches: 659
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-802-285A-2 (1-659) x US-08-258-639A-3 (1-1980)

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RESULT 2
US-08-900-951-3
; Sequence 3, Application US/08900951
; Patent No. 5919693
; GENERAL INFORMATION:
; APPLICANT: Su, Hongsheng
; APPLICANT: Blain, Francoise
; APPLICANT: Bennett, Clark
; APPLICANT: Gu, Kangfu
; APPLICANT: Zimmermann, Joseph
; APPLICANT: Musil, Roy
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,639
; FILING DATE: 10 JUNE 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Healey, William J.
; REGISTRATION NUMBER: 36,160
; REFERENCE/DOCKET NUMBER: 104385.116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942 8400
; TELEFAX: (202)942 8484
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-900-951-3

Alignment Scores:
Pred. No.: 0 Length: 1980
Score: 3494.00 Matches: 659
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-802-285A-2 (1-659) x US-08-900-951-3 (1-1980)

QY 1 MetThrThrLysLeuPheLysArgLeuLeuValPheAlaValLeuSerSerGly 20
Db 1 ATGACTACGAAATTTTAAAGGATCATGTGTTGCTGTAATGGCCCTATCGTCGGA 60
QY 21 AsnLeuLeuAlaGlnSerSerSerLeuThrArgLysAspPheAspHisLeuAsnLeuGlu 40
Db 61 AATATACTTGCAAGGCTCTCCATTACCAAGAAAGATTTTGACCAACATCAACCTTGAG 120

QY 41 TyrSerGlyLeuGluLysValAsnLysAlaValAlaAlaGlyAsnTyrAspAspAlaAla 60
Db 121 TATTCGGACTCGAAAAGGTTAATAAGCAGTTGCTCGCGCAACTATGACGATGCGGC 180
QY 61 LysAlaLeuLeuAlaTyrTyrArgGluLysSerLysAlaArgGluProAspPheSerAsn 80
Db 181 AAAGCATTTACTGGCATACTACAGGGAAGAAAGTAGCCAGGAACTGATTTTCAGTAAT 240
QY 81 AlaGluLysProAlaAspIleArgGlnProLysAspLysValThrArgGluMetAlaAsp 100
Db 241 GCAGAAAAGCCTGCCGATATACGCCAGCCATAGATAGTTACGCGTCAATGGCCGAC 300
QY 101 LysAlaLeuValHisGlnPheGlnProHisLysGlyTyrGlyTyrPheAspTyrGlyLys 120
Db 301 AAAGGCTTTGTCACCCAGTTTCAACCGCACAAAGGCTACGGCTATTTTTCATATGTTAA 360
QY 121 AspIleAsnTyrGlnMetTyrProValLysAspAsnGluValArgTyrGlnLeuHisArg 140
Db 361 GACATCACTGGCAGATGGCCGGTAAAGACAATGAAGTACGCTGGCAGTTGCAACCT 420
QY 141 ValLysTyrTyrGlnAlaMetAlaLeuValTyrHisAlaThrGlyAspGluLysTyrAla 160
Db 421 GTAAAATGCTGGCAGCTATGCGCCCTGTTTATCAGCTACGGCGATGAAAATATGCA 480
QY 161 ArgGluTyrValTyrGlnTyrSerAspTyrAlaArgLysAsnProLeuGlyLeuSerGln 180
Db 481 AGAGAAATGGGTATATCAGTACAGCATTTGGGCGAGAAAACCCATTTGGCGCTGTCGAG 540
QY 181 AspAsnAspLysPheValTyrArgProLeuGluValSerArgValGlnSerLeuPro 200
Db 541 GATATGATTAATTTGTGGCGGCCCTTTGAAGTGTGCGACAGGTACAAAGTCTTCCC 600
QY 201 ProThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMetGluPhe 220
Db 601 CCAACCTTCAGCTTATTTGTAACTCGCCAGCCTTTACCCAGCCTTTTAAATGGAATTT 660
QY 221 LeuAsnSerTyrHisGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGlyAsn 240
Db 661 TTAACACAGTTACCAACACAGCCGATTTATTTATCTACGCATTATGCCGAAACAGGAAAC 720
QY 241 HisArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLys 260
Db 721 CACCGTTTATTTGAAGCCCAACGCACTTTGTTGAGGGGTATCTTCCCTGAAATTTAA 780
QY 261 AspSerProArgTyrArgGlnThrGlyIleSerValLeuAsnThrGluIleLysLysGln 280
Db 781 GATTCAACCAAGATGGAGCAACCCGCATATCGTGTGAACACCGAGATCAAAAACAG 840
QY 281 ValTyrAlaAspGlyMetGlnPheGluLeuSerProLysTyrHisValAlaAlaLeuAsp 300
Db 841 GTTTATGCCGATGGGATGCGATTTGAACCTTCCACAAATTTACCATGTAGTCCCATCGAT 900
QY 301 IlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeuGluLysGluPheProGln 320
Db 901 ATCTTCTTAAGGCTCTATGTTCTGCAAAACAGATTAACTTGAAAAGAAATTTCCGCA 960
QY 321 SerTyrValGlnThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuProAsp 340
Db 961 TCTTATGTACAACTGTAGAAAATATGATTATGGGCTGATCAGTATTTTCACTGCCAGAT 1020
QY 341 TyrAsnThrProMetPheGlyAspSerTyrPheThrAspLysAsnPheArgMetAlaGln 360
Db 1021 TATAACACCCCTATGTTGGAGATTCATGGATTACAGATAAAAAATTTTCAGGATGCAACAG 1080
QY 361 PheAlaSerTyrAlaArgValPheProAlaAsnGlnAlaIleLysTyrPheAlaThrAsp 380
Db 1081 TTTGCGAGCTGGCCCGGTTTCCCGCAACACAGGCCATATAAATATTTTGTACAGAT 1140
QY 381 GlyLysGlnGlyLysAlaProAsnPheLeuSerTyrLysAlaLeuSerAsnAlaGlyPheTyr 400
Db 1141 GCAAAACAAAGGTAAGGCGCTAACTTTTATCCAAAGCATTTGAGCAATGACGGCTTTTAT 1200
QY 401 ThrPheArgSerGlyTyrAspLysAsnAlaThrValMetValLeuLysAlaSerPro 420

Db	1201	ACGTTTAAAGCGGATGGATAAATAATCAACCGTTATGGTATATAAAGCCAGCTCTCTCC	1260
Qy	421	GlyGluPheHisAlaGlnProAspAsnGlyThrPheGluLeuPheIleLysGlyArgAsn	440
Db	1261	GGGGANTTTCATGCCACGCCGATACGGGACTTTTGAACCTTTTATAAAGGCGAGAAAC	1320
Qy	441	PheThrProAspAlaGlyValPheValTyrSerGlyAspGluAlaIleMetLysLeuArg	460
Db	1321	TTTTACCCAGACGCCCGGGGTATTTCTGTATAGCGGCGACGAAGCCCATCATGAACCTCGG	1380
Qy	461	AsnTrpTyrArgGlnThrArgIleHisSerThrLeuThrLeuAspAsnGlnAsnMetVal	480
Db	1381	AACGTGGTACCGTCAAAACCGCATACACACGCTTACACTCGACAAATCAAAATATGGTC	1440
Qy	481	IleThrLysAlaArgGlnAsnLysTrpGluThrGlyAsnAsnLeuAspValLeuThrTyr	500
Db	1441	ATTACCAAAGCCCGCAAAACAAATGGGAAACAGGAAATAACCTTGATGTGCTTACCTAT	1500
Qy	501	ThrAsnProSerTyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsnLysLys	520
Db	1501	ACCAACCAACGCTATCCGAATCTGGACCATCAGCGCAGTGTACTTTTCATCAACAAAAA	1560
Qy	521	TyrPheLeuValIleAspArgAlaIleGlyGluAlaThrGlyAsnLeuGlyValHisTrp	540
Db	1561	TACTTTCTGGTCATCCGATAGGCATATAGCGGAAGCTACCGGAAACCTGGCGGTACACTGG	1620
Qy	541	GlnLeuLysGluAspSerAsnProValPheAspLysThrLysAsnArgValTyrThrThr	560
Db	1621	CAGCTTAAAGAAGACAGCAACCCCTGTTTTCGATTAAGACAAAGAACCGGGTTTACCCACT	1680
Qy	561	TyrArgAspGlyAsnAsnLeuMetIleGlnSerLeuAsnAlaAspArgThrSerLeuAsn	580
Db	1681	TACAGAGATGGTAAACACTGAATGATCCAACTCGTTGAATCGGCACAGGACGAGCTCAAT	1740
Qy	581	GluGluGluGlyLysValSerTyrValTyrAsnLysGluLeuLysArgProAlaPheVal	600
Db	1741	GAAGAAGAAGGAAGGTATCTATGTTTACAATAAGGAGCTGAAAAGACCTGCTTTCGTA	1800
Qy	601	PheGluLysProLysLysAsnAlaGlyThrGlnAsnPheValISerIleValTyrProTyr	620
Db	1801	TTTGAAAAACGCTTAAAGAAATCCCGCATACAGTATCCAGTATAGTTTATCCATAC	1860
Qy	621	AspGlyGlnLysAlaProGluIleSerIleArgGluAsnLysGlyAsnAspPheGluLys	640
Db	1861	GACGGCCAGAGGCTCCAGAGATCAGCATACGGGAAAAACAGGGCAATGATTTTGAAAA	1920
Qy	641	GlyLysLeuAsnLeuThrLeuThrIleAsnGlyLysGlnLeuLeuValLeuValPro	659
Db	1921	GGCAAGCTTAATCTAACCCCTTACCATTACGAAAAACACAGCTTGTTGGTTCTCT	1977

RESULT 3

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1      RESULT 3
2      PCT-US95-07391A-3
3      Sequence 3, Application PC/TUS95507391A
4      GENERAL INFORMATION:
5      APPLICANT: IBEX TECHNOLOGIES and
6      APPLICANT: ZIMMERMANN, Joseph
7      TITLE OF INVENTION: Nucleic Acid Sequences And Expression
8      TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
9      TITLE OF INVENTION: Flavobacterium heparinum
10     NUMBER OF SEQUENCES: 26
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Hale and Dorr
13     STREET: 1455 Pennsylvania Avenue, N.W.
14     CITY: Washington, D.C.
15     COUNTRY: U.S.A.
16     ZIP: 20004
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: Patent In Release #1.0, Version #1.25
22     CURRENT APPLICATION DATA:

```

Db 601 CCAACCTTCAGCTTATTTGTAACCTGCGAGCTTTTACCCCGACCTTTTAAATGGAATTT 660
QY 221 LeuAsnSerTyrHisGlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGlyAsn 240
Db 661 TTAACAGTTACACCAACAGCGCGGNTTATTTATCTACGCAATATGCGCAACAGGGAAC 720
QY 241 HisArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLys 260
Db 721 CACCGTTTATTTGAAGCCCAACGCACTTGTGTCAGGGGTATCTTCCCTGAAATTTAA 780
QY 261 AspSerProArgTyrArgGlnThrGlyIleSerValLeuAsnThrGluIleLysGln 280
Db 781 GAITCACCAGATGGAGGCAACCGGCATATCGGTGCTGAACACCGAGATCAAAAACAG 840
QY 281 ValTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHisValAlaAlaIleAsp 300
Db 841 GTTTATGCGATGGATGAGTTTGAACCTTTCACCAATTTACCATGTAGCTGCCATCGAT 900
QY 301 IlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeuGluLysGluPheProGln 320
Db 901 ATCTTCTTAAAGCCCTATGTTCTGCAAAACGAGTTAACTTGAATAAGAAATTTCCGCAA 960
QY 321 SerTyrValGlnThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuProAsp 340
Db 961 TCTTATGTACAACTGTAGAAATATGATTATGGCGCTGATCAGTATTTCACTGCCAGAT 1020
QY 341 TyrAsnThrProMetPheGlyAspSerTrpIleThrAspLysAsnPheArgMetAlaGln 360
Db 1021 TATAACACCCCTATGTTTGGAGATTCATGATACAGATAAAAAATTTCAAGGATGCCACAG 1080
QY 361 PheAlaSerTrpAlaArgValPheProAlaAsnGlnAlaIleLysTyrPheAlaThrAsp 380
Db 1081 TTTGCGAGCTGGCGCGGTTTTCGCGCAACACGAGCCCATATAATTTTGTCTACAGAT 1140
QY 381 GlyLysGlnGlyLysAlaProAsnPheLeuSerLysAlaLeuSerAsnAlaGlyPheTyr 400
Db 1141 GGCNAACAGGTAAAGCGCTAACTTTTATCCAAAGCAITGAGCAATGACGCTTTTAT 1200
QY 401 ThrPheArgSerGlyTrpAspLysAsnAlaThrValMetValLeuLysAlaSerProPro 420
Db 1201 ACGTTTAGAGCGGATGGGATAAAATGCAACCGTTATGGTATTAAGCCAGTCTCTCC 1260
QY 421 GlyGluPheHisAlaGlnProAspAsnGlyThrPheGluLeuPheIleLysGlyArgAsn 440
Db 1261 GGGGAATTTTCATGCCAGCGGATACGGGACTTTTGAACCTTTTATAAAGGCGCAGAAAC 1320
QY 441 PheThrProAspAlaGlyValPheValTyrSerGlyAspGluAlaIleMetLysLeuArg 460
Db 1321 TTTACCCAGACGCGGGGTATTTGTATAGCGGCGAGAGCCATCATGAACTGCCG 1380
QY 461 AsnTrpTyrArgGlnThrArgIleHisSerThrLeuThrLeuAspAsnGlnAsnMetVal 480
Db 1381 AACTGTGACCGTCAAAACCCGATACACAGACGCTTACACTCGACAATCAAAATATGTC 1440
QY 481 IleThrLysAlaArgGlnAsnLysTrpGluThrGlyAsnLeuAspValLeuThrTyr 500
Db 1441 ATTACAAAGCCGCGCAAAACAAATGGGAAACAGGAAATAAAGCTGATGTCTTACCTAT 1500
QY 501 ThrAsnProSerTyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsnLysLys 520
Db 1501 ACCNACCCAGCTATCCGAACTTGGACCATCAGCGAGTGTACTTTTCATCAACAAAAA 1560
QY 521 TyrPheLeuValIleAspArgAlaIleGlyGluAlaThrGlyAsnLeuGlyValHisTrp 540
Db 1561 TACTTTCTGTCATCATGATAGGCAATAGCGAAGCTACCGGAAACCTGGCGGTACACTCG 1620
QY 541 GlnLeuLysGluAspSerAsnProValPheAspLysThrLysAsnArgValTyrThrThr 560
Db 1621 CAGCTTAAAGAGACAGACACCTGTTTTCGATTAAGCAAAAGAACCGGGTTTACACCACT 1680
QY 561 TyrArgAspGlyAsnAsnLeuMetIleGlnSerLeuAlaAspArgThrSerLeuAsn 580

Db 1681 TACAGAGATGGTAACAACCTGATGATCCATCTTGAATGCCAGACGACCTCAAT 1740
QY 581 GluGluGluGlyLysValSerTyrValTyrAsnLysGluLeuLysArgProAlaPheVal 600
Db 1741 GAAGAAGAAGGAAGGTATCTTATGTTTACATAAAGGAGCTGAAAAAGACCTGCTTCGTA 1800
QY 601 PheGluLysProLysLysAsnAlaGlyThrGlnAsnPheValSerIleValTyrProTyr 620
Db 1801 TTTGAAAAAGCTTAAAAAAGAAATCCGCGCACACAAAAATTTTGTGATATAGTTTATCCATAC 1860
QY 621 AspGlyGlnLysAlaProGluIleSerIleArgGluAsnLysGlyAsnAspPheGluLys 640
Db 1861 GACGCCAGAGGCTCCAGAGATCAGCATACGGGAAACAAAGGCAATGATTTTGAGAA 1920
QY 641 GlyLysLeuAsnLeuThrLeuThrIleAsnGlyLysGlnGlnLeuValLeuValPro 659
Db 1921 GGCAAGCTTAATCTTAACCCCTTACCATTACGAGAAACCAACAGCTTGTGTGTTCTCT 1977

RESULT 4

US-08-961-527-186/c
; Sequence 186, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-186

Alignment Scores:

Pred. No.: 9,81e-10 Length: 3763
Score: 176.00 Matches: 116
Percent Similarity: 34.63% Conservative: 80
Best Local Similarity: 20.49% Mismatches: 231
Query Match: 5.04% Indels: 140
DB: 4 Gaps: 20

US-09-802-285A-2 (1-659) x US-08-961-527-186 (1-3763)

QY 71 SerLysAlaArgGluProAspPheSerAsnAlaGluLysProAlaAspIleArgGlnPro 90
Db 2173 TCAAAAGACTATGAGAAAGTCAAGAGTTCCCTTTGAACGCTTGATGACAAATCGTTTATG 2114

Db 208 AAAGAGTATCGGTGGAAATCGGTATCCGTATCGATGATGATCCAGATGGCTCTTTATGTTGAGT 267
Qy 140 ArgValValThrProGlnAlaMetAlaLeuValTyrHisAlaThrGlyAspGluTyr 159
Db 268 CGTCAAAAGCTTTCTGTAGATCTGGCACAAGCATATGCACTTACTAAAAAGAACGTTAC 327
Qy 160 AlaArgGluThrProGlnTyrSerAspTyrAlaArgLysAsnProLeuGlyLeuSer 179
Db 328 TTACAGAAATGGCAGACTTGTCTTATTTGATTTTATT-----AACGATGAGGTGAGCCA 381
Qy 180 GlnAspAsnAspLysPheValTyrArgProLeuGluValSerAspArgValGlnSerLeu 199
Db 382 AATTCACGATAGGATGTTGGCGTCCGTAGATGTTGGGATTCGAGTAAACAAC----438
Qy 200 ProProThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMetGlu 219
Db 439 -----TGGATGAAAGCTTCACGTATATTTCCATTCGCTGATTTTCAGA 480
Qy 220 PheLeu-----AnSerTyrHisGlnGlnAlaAspTyrLeuSer 232
Db 481 CTATTAGGAATGATGATGTTGAAACGCTTCGTGATCCATCTGGCATTTTGGAG 540
Qy 233 ThrHisTyrAlaGluGlnGlyAsnHisArgLeuPheGlu-----245
Db 541 CGGTCTATATCGATAAA-----TACAGCTCAGTAATTTGGGCTGTGTTGGCAATGGT 594
Qy 246 -----AlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLysAspSerPro 263
Db 595 GGAATGGCAGCTATTGATTTATTT-----CTTCCAGAACTGGTGACCACT---639
Qy 264 ArgTyrArgGlnThrGlyLeuSerValLeuAsnThrGluLeuLysGlnValTyrAla 283
Db 640 AAACAGAGGATCAATATATGCTCTGTTAGCTGAACAGCTGATCAACAATTTCTATTCA 699
Qy 284 AspGlyMetGlnPheGluLeuSerProIleTyrHisValAlaAlaIleAspIlePheLeu 303
Db 700 GATGNAATTCATGGAGCAGAGCCCGCTGTAC-----732
Qy 304 LysAlaTyrGlySerAlaLysArgValAsnLeuGluLysGluPheProGlnSerTyrVal 323
Db 733 -----CAGCAGAAAGTTTGTGATGACATTCGTG 759
Qy 324 GlnThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuPro-----339
Db 760 TATCTATTCGAG-----ATTCTGAATATCTGAAGTCGAGTACCATTTAGATCTTCGC 813
Qy 340 ---AspTyrAsnThrProMetPheGlyAspSerTyrIleThrAspLys-----354
Db 814 ATCAAAATTAACAACACTATTCTCTACCCATTATTTGGCGGATAACCAAGATATCCCTA 873
Qy 355 -----AsnPhe-----356
Db 874 AATCCGATCAATGATGATCATGTCACCTTTTCATTAGCTATATGATATCTATCGCAAA 933
Qy 357 -----ArgMetAlaGlnPheAlaSerTyrAla 365
Db 934 TTAGTGTTCATATTGAACCTCCATGACTGCGAATATGCAAGCGTT-----TGGAGC 987
Qy 366 -----ArgValPheProAlaAsnGlnAlaIleLysTyrPheAla---378
Db 988 GGGGATCTTTATGAAGAAAGATCTGGGAAAC-AATGAAGCCAAAAGAACTTTTTCGTGG 1046
Qy 379 -----ThrAspGlyLysGlnGlyLeuAlaProAsnPheLeuSerLysAlaLeu 394
Db 1047 CGAATCAAGTGGGCTGATGGCGTACAAAGCAGA-----GGATATCTA-----1088
Qy 395 SerAsnAlaGlyPheTyrThrPhe---ArgSerGlyTyrAspLysAsnAlaThrValMet 413
Db 1089 -----TTTATACCTTTTAACTGCTGCTGATGG-----1115
Qy 414 ValLeuLysAlaSerProGlyGlu-PheHisAlaGlnProAspAsnGlyThrPheGlu 433
Db 1116 -----GAGCGCACATGGTCTCTCTACAGTGATTTAC 1151

Qy 433 uLeuPheIleLysGlyArgAsnPheThrProAspAlaGlyValPheValTyrSerGlyAs 453
Db 1152 ACTCAACATACAAAGGGATCACTTATTTCCGATAGTGGTTCGATTACAGCTATGTCAACA 1211
Qy 453 pGluAlaIleMetLysLeuArgAsnTyrTyrArgGlnThrArgIleHisSerThrLeuTh 473
Db 1212 ATCAGAGCGACTTCAGCTA-----AAAGAGTGGCTTCGACAATACGATGTT 1259
Qy 473 rLeu---AspAsnGlnAsnMetValIleThr-----LysAlaArgGlu 486
Db 1260 TATCGCGAATAATCCCATACCTTATTTCCGATAGTGGGTTATGACAAATTACCGAC 1319
Qy 486 nAsnLysTyrGluThrGlyAsnLeuAspValLeuThrTyrThrAsnProSerTyrPr 506
Db 1320 ACCCTTATTTCCAGAAATAAAAGAACTTCTGTGCGTTTTTTTTCGAGAATGCGGCTGGCT 1379
Qy 506 oAsnLeuAspHisGlnArgSerValLeuPheIleAsnLysLysTyrPheLeu-----523
Db 1380 GGATAAGCGGATCCAGATCCCAATGATTTTTCGAGCGCAGCTTCATCTATTTAAAGTCGAT 1439
Qy 524 -----ValIleAspArgAlaIleGlyGlu-----AlaTh 533
Db 1440 CAACTCCGTAGTTATTTATTTAGTAGCTTTCGAGGACAGAAAGACTGAAATTACGAGTAC 1499
Qy 533 rGlyAsnLeuGlyValHisTyrGlnLeuLysGluAspSerAsnProValPheAspLysTh 553
Db 1500 CTATATTTGGCAGCGCTCGATTAATTTGTCAAAAAGAGCGCATCGGTTTTCCTTAACTAC 1559
Qy 553 rLysAsnArgValTyrThrTyrArgAspGlyAsnLeuMetIleGlnSerLeuAs 573
Db 1560 GAACAGCATAAGTACACACTCTCTTTTCTGCTGGAGGC-----1596
Qy 573 nAlaAspArgThrSerLeuAsnGluGluGlyLysValSerTyrValTyrAsnLysGlu 593
Db 1597 -----CAAACACAGCAATCAGTGGCAAAAGGTTTCAGAGATTTATAACCACT 1643
Qy 593 uLeuLysArgPro-----AlaPheValPheGluLysProLysLysAsnAlaGlu 609
Db 1644 GAATGAGCACCCGACGCTTATCAACAAAGTTTGTTCACAAAACGGG-AAAAGAAATTCAAG 1702
Qy 609 YThrGlnAsnPheValSerIleValTyrProTyrAspGlyGlnLysAla 625
Db 1703 CAAAGCTCAITTCCTCGTTAGAGGATATCCAAATTACGCCAATAAAGT 1751

RESULT 6

US-09-134-001C-795
; Sequence 795, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 795
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-795

Alignment Scores: 4,46e-05 Length: 2097
Pred. No.: 132.50 Matches: 140
Score: 34.59% Conservative: 108
Best Local Similarity: 19.53% Mismatches: 260
Query Match: 3.79% Indels: 210

DB:	4	Gaps:	30
US-09-802-285A-2 (1-659) x US-09-134-001C-795 (1-2097)			
QY	9	IleIleValPheAlaValIleAlaLeuSerSerGlyAsnIleLeuAlaGlnSerSer	27
DB	94	GTATTTATCTTGGCTATAGTCGATTTCAGATTAGGTTATTTACAAATAGCACAGGATCT	153
QY	28	SerIleThrArgLysAspPheAspHisIleAsnLeuGluTyrSerGlyLeuGlu	45
DB	154	CATTACAAACAATTAATCAAAACCGATGAAACATAACT	192
QY	46	LysValAsnLysAlaValAlaAlaGlyAsnTyr	56
DB	193	---GTTAATGAATCAGTACCAAGAGGCGGAATACTAGATGAAATGGCAAGTACTAGTT	249
QY	57	AspAlaAlaLysAlaLeuLeuAlaTyrTyrArgGluLysSerLysAlaArgGluPro	76
DB	250	GATAATGCTTCAAAAGATGCTATTACATACACTAGAAACCGTAAACCATCACAAAGAA	309
QY	77	AspPheSerAsnAlaGluLysProAlaAspIleArgGlnProIleAspLysValThr	95
DB	310	ATGTTAAATACTGCTAAAGAACTGACAGATTTAATTAATAATGGATACAGATAAAATTACT	369
QY	96	ArgGluMetAlaAspLysAlaLeuValHisGlnPheGlnProHisLysGlyTyrGlyTyr	115
DB	370	GAGAGA---GATAA	381
QY	116	PheAspTyrGlyLysAspIleAsnTrpGlnMetTrpProValLysAspAsn	132
DB	382	---AAGGATTTTGGATTCAAATGTATCCGTCATTTGCTAATAAAGTT-AAAT	428
QY	133	GluValArgTrpGlnLeuHisArgValLysTrpTrpGln	145
DB	429	GAGAAAGA---ACAAATTAATGTTAGAGGATGGCAGTATTTCAACAGCAATTTGA	482
QY	146	---AlaMet	147
DB	483	TACCCAACTTAGAGATAAAATAGGAAAAAACAATTAACAAGTTAACTAAAAAGATT	542
QY	148	AlaLeuValTyrHisAlaThrGlyAspGluLysTyrAla	160
DB	543	GCAAGTTTTAGCAATTTATCGGAAATGAACGCTGGGTCAACTCTAGATCCTCAAAACAAT	602
QY	161	---ArgGlu	162
DB	603	TAAAAATGAAGACGTACGCGAGAAAGAAATATGCACCGTATCACACAGCTTCTAAAT	662
QY	163	---TrpValTyrGlnTyrSerAspTrpAlaArgLysAsnProLeuGlyLeuSerGlnAs	181
DB	663	ACCTGGTGTAAATACTACAATGATTTGGGATAGAAATACCCATACGCT	713
QY	181	pAsnAspLysPheValTrpArgProLeuGluValSerAspArgValGlnSerLeuProPr	201
DB	714	TACTTTAAGGCATATTTGA---GATGTGCACTTCGACTGAAGGTATACCTAA	767
QY	201	oThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMetGluPheLe	221
DB	768	AGAATTAAC	788
QY	221	uAsnSerTyrHisGlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGlyAsnHi	241
DB	789	ATCAAAAGGTTATTCAGAAATGATCGGGTCGGTAAATCTTCTTGAATATCAATACGA	848
QY	241	sArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSerPheProGluPheLysAs	261
DB	849	AGATGTTCTTAAAGCGACGAAAGAAACAATG	890
QY	261	pSerProArgTrpArgGlnThrGlyIleSerValLeuAsnThrGluIleLysLysGlnVa	281
DB	891	TGATAAATCTCGAAGGATTAAGTTGCAAGTACTTAAATCCTGGCTCAAGA	942
QY	281	lTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHisValAlaAlaIleAspIl	301

Db 1887 CGGAGAACTAGAGTTAACTCAACAT---ATATCGTTATGACCCG 1930

RESULT 7

US-07-973-320-1
 ; Sequence 1, Application US/07973320
 ; Patent No. 5286486
 ; GENERAL INFORMATION:
 ; APPLICANT: Payne, Jewel M.
 ; APPLICANT: Fu, Jenny M.
 ; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
 ; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/973,320
 ; FILING DATE: 19921106
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/788,638
 ; FILING DATE: 6-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: MA68.C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3414 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bacillus thuringiensis
 ; STRAIN: dakota
 ; INDIVIDUAL ISOLATE: HD511
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Lamdagem (TM)-11 library of J.M. Fu
 ; CLONE: 511
 ; US-07-973-320-1

Alignment Scores:

Pred. No.: 0.0011 Length: 3414
 Score: 123.50 Matches: 141
 Percent Similarity: 35.92% Conservative: 95
 Best Local Similarity: 21.46% Mismatches: 199
 Query Match: 3.53% Indels: 224
 DB: 1 Gaps: 39

US-09-802-285A-2 (1-659) x US-07-973-320-1 (1-3414)

QY 48 AsnLysAlaValAla-----AlaGlyAsnTyrAspAlaAlaLysAlaLeu 63
 Db 361 AATAAGACCTTCGAGAAATAGAGGATTTAGGAAATAAC----- 399
 QY 64 LeuAlaTyrTyrArgGluLysSerLysAlaArgGluProAspPheSerAsnAlaGluLys 83
 Db 400 TTAACAATATATCAACAG-----GCACTTGAAGATTGGCTGAACAACTCCTGATGAT 450

QY 84 ProAlaAspIleArgGlnProIleAspLysValThrArgGluMetAlaAspLysAlaLeu 103
 Db 451 CCAGCACTATAACACAGAGTGTATAGTCTTTT-----CGTATATTAGAT---GCTTTA 501
 QY 104 ValHisGlnPheGlnProHisLysGlyTyrGlyTyrPheAsp----- 117
 Db 502 TTTGAATCATATATGCCGTCAATTAGGGTTGCTGGATATGAAATACCATTAACAGTT 561
 QY 118 TyrGlyLysAspIleAsnTrpGlnMet----- 126
 Db 562 TAGCACAAGCGGCAACCTTCATCTAGCTTTATTAAAGAGATTCTACTCTTTATGGAGAT 621
 QY 127 ---TrpProValLysAspAsnGluVal----- 134
 Db 622 AAATGGGATTCACATCAGAACCAACATTCAGGAAAAATTAAATCGTCAAAAGAAACATATC 681
 QY 135 ---ArgTrpGlnLeuHisArgValLysTrpTrpGlnAla---MetAlaLeuValTyrHis 152
 Db 682 TCTGAATATTCTAACCATTCGCTTAAGTGTATATAGTGTCTTAGCAGATTGAACGGT 741
 QY 153 AlaThrGlyAspGlu-----LysTyrAlaArgGluTrpValTyrGlnTyr 167
 Db 742 TCCACTTATGAACAATGGATAAATTATAATCGTTTTCTGAGAGAAATGATATTAAATGGA 801
 QY 168 SerAspTrpAlaArgLysAsnProLeu-----GlyLeu 178
 Db 802 TTAGATATTGCTGCTGTATTTCCTATTATGACCCCTCGAATGTATTTCATGAAACAACT 861
 QY 179 SerGlnAspAsnAspLysPheValTrpArg-ProLeuGluValSerAspArgValGlnSe 198
 Db 862 AGCAGTT-AACGAGAGAGTGTATACCATCAATTAGCTTGTCAATTAGCAATCCAGA 920
 QY 198 rLeuProThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMe 218
 Db 921 TATAGTCCAGCTTTTCTCAGATGGAATAATCTGCGTTTAGAACACACACCTTGT-- 978
 QY 218 cGluPheLeuAsnSerTyrHisGlnAlaAspTyrLeuSerThrHisTyrAlaGlu 238
 Db 979 -----GATTATTAGATGAGCTTTATATATATATAC 1007
 QY 238 nGlyAsnHisArgLeuPhe-----GluAlaGlnArgAsnLeuPhe-----Al 252
 Db 1008 ATCAAAATATAAGCATTTTCATGAGATTCAACAGACCTATTTTATTGTTGTGTACA 1067
 QY 252 aGlyValSerPheProGluPheLysAspSerProArgTrpArgGlnThrGlyLe-SerV 272
 Db 1068 TAAGGTTAGCTTTAAAAAATCGAGCAATCCCAATTATATAT---ACAACAGGCATATATGG 1124
 QY 272 alLeuAsnThrGluLe-----LysLysGlnValTyrAlaAspGlyMet---GlnPheG 289
 Db 1125 TAAACAAAGTGGATATATTTTCATCAGGAGCATATTCATTTAGAGGAATGATATCTATAG 1184
 QY 289 luLeuSerProIleTyrHisValAlaAlaIleAspIlePheLeuLysAlaTyrGlySerA 309
 Db 1185 AACATTAGCAGCTCCATCAGTTGTAGTTTATCCGTATA---CTCAGAATTATGTTGTGCA 1241
 QY 309 laLys----- 310
 Db 1242 GCAAGTTGAGTTTACGGTGTAAAGGGCATCTACATTATAGAGGAGATAACAAATATGA 1301
 QY 311 ----ArgValAsnLeuGluLysGluPheProGlnSerTyrValGlnThrValGluAsnM 329
 Db 1302 TCTGAGGTATGATTCTTATGATCAATACCCAGGAGAACCAATACACGAAATAA 1361
 QY 329 etIleMetAlaLeu-----IleSerIleSerLeuProAspTyrAsnThr- 343
 Db 1362 CACTCATCGA-TTATGTCTATGCTACAGCTATATCTAAATCAACTCCGGATTATGATAATG 1420
 QY 344 -----ProMetPheGlyAspSerTrpIleThrAspLysAsnPheArgMetAlaGlnP 361
 Db 1421 CTACTATCCGATCTTT-----TCTTGG-----ACGCATAGAGTGGGAGT 1462


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QY 361 heaLaSerTrpAlaArgValPheProAlaasn-----GlnAlaIleLysTyrP 377
Db 1463 AT-----TACAATAGAACTATCCAAACAAAATCAAAAAATTCACAGCTGTAAAAATGT 1516
QY 377 heaLaThrAspGlyLysGlnGly-----LysAlaProAsnPhelSerLysAlaLeuS 395
Db 1517 ATAACTAGATGATCTATCTACAGTTGTCAAGGGCTGGATTACAGGTGAGATTAG 1576
QY 395 erAsnAlaGlyPheTyrThrPheArgSerGlyTrp-----AspLysAsnAlaThrValm 413
Db 1577 TTAAGAGAGGG-----AGTAATGTTTATATAGGAGATATAAAGGCTACCGTA- 1623
QY 413 etValLeuLysAlaSerProProGlyGlu-----PheHisAlaGlnP 427
Db 1624 -----AACTCACCACTTCTCAAAAATATCGTGTAGAGTTCGATACCCACTA 1672
QY 427 roAspAsnGlyThrPheGluLeuPheIleLysGlyArgAsnPhelThrProAspAlaGlyV 447
Db 1673 GTGTTTCTGGACTATTCAACGTGTTTATT-----1701
QY 447 alPheValTyrSerGlyAspGluAlaIleMetLysLeuArgAsnTrpTyrArgGlnThrA 467
Db 1701 -----1701
QY 467 rgIleHisSerThrLeuThrLeuAspAsnGlnAsnMetValIleThrLysAlaArgGlnA 487
Db 1702 -----AATGATGAATAGCGCTTCAAAAAAATTTTCAA 1735
QY 487 snLysTrpGluThr-----GlyAsnAsnLeuAspValLeuThrTyr-----500
Db 1736 GTACTGTAGAAACAATAGGTGAAGAAAGAT-----TTAACCTATGTTTCATTGGATATA 1792
QY 501 -----ThrAsnProSerTyrProAsn-----LeuA 509
Db 1793 TAGAATATCTCAGACCACTCAATTTCCGAATGAGATCCAAAAATCCTCTTCATTAA 1852
QY 509 spHis-----GlnArgSerValLeuPheIleAsnLysLysTyrPheLeuValIleAspA 527
Db 1853 ACCATTGAGTAACAATTCACCATTTATGTAGATTCATCGAATTTATCCCTGTAGAT- 1911
QY 527 rgAlaIleGlyGluAlaThrGlyAsnLeuGlyValHisTrpGlnLeuLysGluAspSerA 547
Db 1912 -----GTAAATATTGATGAAAAAGAAAAA-----1935
QY 547 snProValPheAspLysThrLysAsnArgValTyrThrTyrArgAspGlyAsnAsnL 567
Db 1936 -----CTAGAAAAAGCAGAAAGCCGGGAATACCTGTTTACAGAGGAGAAATG 1987
QY 567 euMet-----IleGlnSerLeuAsnAlaAspArgThrSerLeu 579
Db 1988 CACTCCAAAAATAGTGCACAGATTATATAAGTGGACCAAGTTTCAATT 2034
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RESULT 8

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US-08-328-962-1
; Sequence 1, Application US/08328962
; Patent No. 5536637
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; TITLE OF INVENTION: A NOVEL METHOD FOR ISOLATING CYTOKINES
; TITLE OF INVENTION: AND OTHER SECRETED PROTEINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,962
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,267
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; IMMEDIATE SOURCE:
; CLONE: SUC2
; US-08-328-962-1
Alignment Scores:
Pred. No.: 0.000346 Length: 1542
Score: 123.00 Matches: 109
Percent Similarity: 32.01% Conservative: 76
Best Local Similarity: 18.86% Mismatches: 179
Query Match: 3.52% Indels: 214
DB: 1 Gaps: 31
US-09-802-285a-2 (1-659) x US-08-328-962-1 (1-1542)
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QY 94 ValThrArgGluMetAlaAspLysAlaLeuValHisGlnPheGlnProHisLysGlyTyr 113
Db 4 ATGACAAACGAAACTAGCATAGACCTTTGGTCCAC---TTCCACCCCAACAGGGCTGG 60
QY 114 -----GlyTyrPheAspTyrGlyLysAspIleAsnTrpGlnMetTrp---127
Db 61 ATGATGACCAAAATGGTTGGTACGATGAAAAGATGCCAATGGCATCTGTACTTT 120
QY 128 ProValLysAspAsnGluValArgTrpGlnLeuHisArgValLysTrpTrpGlnAlaMet 147
Db 121 CAATACAAACCAAAATGACACCGTATGG-----GGTACGCCATTGTTTGGGGC-----168
QY 148 AlaLeuValTyrHisAlaThrGlyAspGluLysTyrAlaArgGluTrpValTyrGlnTyr 167
Db 169 -----CATGCTACTTCCGATGAT-----TTG 189
QY 168 SerAspTrpAlaArgLysAsnProLeuGlyLeuSerGlnAspAsnAspLysPheValTrp 187
Db 190 ACTAATTTGG---GAAGATCAACCACTTGTCTCGCTCCCAAGCGTAAC-----234
QY 188 ArgProLeuGluValSerAspArgValGlnSerLeuProThrPheSerLeuPheVal 207
Db 234 -----234
QY 208 AsnSerProAlaPheThrProAlaPheLeuMetGluPhe-----220
Db 235 GATTCAGTGCTTTCTCTGCTCCATGGTGGTGGATTACAAACACAGCAGTGGGTTTTC 294
QY 221 -----LeuAsnSerTyrHis 225
Db 295 AATGATACTATTGATCCAGACAAAGATGGTGGCGATTGGCGATTATGACTTATAACTCTCTGAA 354
QY 226 GlnGlnAlaAspTyrLeuSerThrHisTyrAlaGluGlnGlyAsnHisArgLeuPheGlu 245
Db 355 AGTGAAGCAATACATTAGC-----TATTCTTGTGATGGTGTACTTTACTGAA 408
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QY 341 ---TyrAsnThrProMetPheGlyAspSerTrpIleThrAspLysAsnPheArgMetAla 359
 Db 3684030 TTCGACGAGAACCGATGACGACGACCACTTTCGTG----- 3683995
 QY 360 GlnPheAlaSerTrpAlaArgValPheProAlaAsnGlnAla-----Ile 374
 Db 3683994 -----CGGACCTTCGACGCGCTGACGCGGAAAGACCGCCACACCGTG 3683953
 QY 375 LysTyrPheAlaThrAspGlyLysGlnGlyLysAlaProAsnPheLeuSerLysAlaLeu 394
 Db 3683952 CAGTACTTC-----GAAACTTCGGCAGCGTGCCATC 3683920
 QY 395 SerAsnAlaGlyPheTyrThrPhe-----ArgSerGlyTrpAspLysAsnAla 410
 Db 3683919 TACAAAGACGGTGTGGCGTGGCGTGGACAGCGCCCTGGGATCTGTCAACG 3683860
 QY 411 ThrValMetValLeuLysAlaSerProProGlyGluPheHisAlaGlnProAspAsnGly 430
 Db 3683859 GAGACGATG-----CGACGGTTCGGCGCGGGGACCTAC-----GACCCGACCAAGGAC 3683812
 QY 431 ThrPheGluLeuPheIleLysGlyArgAsnPheThrProAspAlaGlyValPheValTyr 450
 Db 3683811 GTCGGGACTGTACTACCTACGATGACTCTCCAGCGGAAACCTGGCAGCGGAG 3683752
 QY 451 SerGlyAspGluAlaIleMetLysLeuArgAsnTrpTyrArgGlnThrArgIleHisSer 470
 Db 3683751 CATCCCGACAGGTGCGCGAGCTCACCCAGCTGTGGTGGCAGGCGCGAAACGACCGG 3683692
 QY 471 ThrLeuThrLeu 474
 Db 3683691 GTGCTGCGCGCTG 3683680

RESULT 11

US-09-543-681A-3009
 ; Sequence 3009 Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709,1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 3009
 ; LENGTH: 3087
 ; TYPE: DNA
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-3009

Alignment Scores:

Pred. No.:	0.00468	Length:	3087
Score:	117.50	Matches:	167
Percent Similarity:	32.80%	Conservative:	101
Best local Similarity:	20.44%	Mismatches:	280
Query Match:	3.36%	Indels:	269
DB:	4	Gaps:	49

US-09-802-285A-2 (1-659) x US-09-543-681A-3009 (1-3087)

QY 5 IlePheLysArgIleIleValPheAlaValIleAlaLeuSerSerGlyAsnIleLeuAla 24
 Db 817 ATCGACAAATTTAGCATTTAGGAAAAATTTAGCCTTAGAACAA-----CAT 864
 QY 25 GlnSerSerIleThrArgLysAspPheAspHisIleAsn-----LeuGlu 40
 Db 865 GCTGATGGCTCAATAACCCGAAAGCCCTTGATCATCTTAATCGCCAGAAATTTTATCAA 924
 QY 41 TyrSerGlyLeu-----GluLysValAsnLysAlaValAlaAlaGlyAsn---TyrAsp 57

Db 925 GTCGAGGGGGTCTTTAGTGAAGAAACCCAAAAAGCATTTACTTGATGCCAACATGCTTAAGA 984
 QY 58 AspAlaAlaLysAlaLeuLeu-----AlaTyrTyrArgGlnLysSerLysAlaArg 74
 Db 985 GATGTAGGCAAAACGCTTCTTCAACAGCGATTTACTTGGTAGTCGCTCCTTATCA---1041
 QY 75 GluProAspPheSerAsnAlaGluLysProAlaAspIleArgGlnProIleAspLysVal 94
 Db 1042 -----GCAATCGATAGAAAAAATTTAGAACGCTC 1071
 QY 95 -----ThrArgGluMetAlaAspLysAlaLeuVal-----HisGln 106
 Db 1072 TATTTATTTAGGCACCTGTTACGTTCTTGAACAAGGTTTCCACCGGGAGTGGTTACCAA 1131
 QY 107 PheGlnProHisLysGlyTyr-----GlyTyrPheAsp-----TyrGlyLys 120
 Db 1132 ATTATTTACTCAGTAGTTATCAACACAGAGAGCTTTTGTATGCATGGTTTATTGTCGC 1191
 QY 121 AspIle-----AsnTrpGlnMetTrpPro---128
 Db 1192 CATATTCTAGCAAAACATAATCTGTGTAGCACCGACACAAACAGCCATGATGTGTATAAC 1251
 QY 129 -----ValLysAspAsnGluVal-----134
 Db 1252 GCAACAGCGCGCATATTGAAAAAGATAATGAATCGTTGTGCAAAATGTCGATATTCTC 1311
 QY 135 ArgTrpGlnLeuHisArgValLysTrpTrpGlnAlaMetAlaLeuValTyrHisAlaThr 154
 Db 1312 AATACCAATTACAG-----TGGATATAAAAGTTTATTG-----ATGTTG 1353
 QY 155 GlyAspGluLysTyrAlaArgGluTrpValTyrGlnTyrSerAspTrpAlaArgLysAsn 174
 Db 1354 CCAGATTATCAACAGCGCCACCAAGCCTTAGCACAAATTCGAAAGTTGGCTAACCAAAACC 1413
 QY 175 ProLeu-----GlyLeuSerGlnAspAsnAspLysPhe-----185
 Db 1414 ATTTAGTTCTAAAGGTGTCGCTGGCTTTAAATCTGATGGCTCTATTTTTCACCAT 1473
 QY 186 ---ValTrpArgProLeuGluValSerAspArgValGlnSerLeuProProThrPheSer 204
 Db 1474 TCACAACATTATCCAGCTTATCCAAAGATGCATTTGGTGGCTTAGCGCTAGTGTATTAT 1533
 QY 205 LeuPheValAsnSerPro-----AlaPheThrProAla-----215
 Db 1534 GCCTTAAGTCATTCCTCCCTTTTCGCTTTTCATCACCAGCACATGCACGCTTAAAGATGTA 1593
 QY 216 PheLeuMetGluPheLeuAsnSerTyrHisGlnGlnAlaAspTyrLeuSerThrHisTyr 235
 Db 1594 TTATTAATAATCGGTATCTATACCAAGAAACACAAATTCCTCTGCTGTTAATAGTGCAGA 1653
 QY 236 AlaGluGlnGlyAsnHisArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSer 255
 Db 1654 CATCTACGGGGTTACATAA-----ATAAGT 1680
 QY 256 PheProGluPheLysAspSerProArgTrpArgGlnThrGlyIleSerValLeuAsnThr 275
 Db 1681 ATTGATCCCTTCAAA-----TGG-----ATGCTCTTCAGGATAG 1716
 QY 276 GluIleLysLysGlnValTyrAlaAspGlyMetGlnPheGluLeuSerProIleTyrHis 295
 Db 1717 -----CCCGATGGTAACAA---GAGCTAGATACTACA-----1746
 QY 296 ValAlaAlaIleAspIlePheLeuLysAlaTyrGlySerAlaLysArgValAsnLeuGlu 315
 Db 1747 TTAGCAGCGCTTATGCAAAATTTAGCAACAAAGATAGCTTTGAAGGTATTAAACGAGAA 1806
 QY 316 LysGluPheProGlnSerTyrValGlnThrValGluAsnMet---IleMetAlaLeuIle 334
 Db 1807 AATGACCGGTAGGTGTCATGGGCAATGAATTTATGTTCAATGGCAATCCAGCGTAGACA 1866
 QY 335 SerIleSerLeuProAspTyrAsnThrProMetPheGlyAspSerTrpIleThrAspLys 354
 Db 1867 TCATTAACAGGCCACAG-----CAAAAGCTGG-----1893

Qy 355 AsnPheArgMetAlaGlnPheAlaSerTrpAlaArgValPheProAlaAsnGlnAlaIle 374
Db 1894 -----CTTGCTATCGCTCGGTTTTAGTCGTTATTAGTGGGTAATGAAAGT--- 1941
Qy 375 LysTyrPheAlaThrAspGlyLysGlnGlyLysAlaProAsnPhe----- 389
Db 1942 -----TATGAGATAACAACCGTTATGGTCGTTACTTGCNATATGGCAACTTGAATT 1995
Qy 390 LeuSerLysAlaLeuSerAsnAlaGlyPheTyrThrPheArgSerGlyTrpAspLysAsn 409
Db 1996 ATTCCTCGGATTTAACTAAATCTGGTTTT-----AGTCATGCAGGTGGGATTGGAAT 2049
Qy 410 -----AlaThrValMetValLeuLysAlaSerProGlyGluPheHisAla 425
Db 2050 CGATATCCAGGAACGACTACGACTCCACCTT-----CCTATGATGAACACTAGAAGCA 2100
Qy 426 Gln-----ProAspAsnGlyThrPheGluLeuPheIleLysGlyArgAsnPhe 441
Db 2101 AAATAAGCCNATTCGCAAGTCAGGATAGAGAATAATGTTGCTTCAACACACGTT--- 2157
Qy 442 ThrProAspAlaGlyValPheValTyrSerGlyAspGluAlaIle----- 456
Db 2158 -----TATTCGTGTCCTCAATACACATAACATAATAATAACAGTATG 2193
Qy 457 -----MetLysLeu-----ArgAsnTrpTyrArgGlnThrArgIleHis----- 469
Db 2194 TTTCCCATGAATTAACATGTCACAGTAATATCAACAACAAAGTCTAAGAGCGAATAAA 2253
Qy 470 SerThrLeuThrLeuAspAsn-----TATTCGTGTCCTCAATACAGTATG 2313
Db 2254 TCCTATTCTTATTGATAATAGATGATCGCATAGGCTCTGGTATTGAAATAACGAT 2373
Qy 477 -----GlnAsnMet 479
Db 2314 AAACAACATACACAGAAACGACACTGTTCCAGTTGCTGTTCTTAAGTTACATCAATT 2373
Qy 480 ValIleThrLysAlaArgGlnAsnLysTrpGluThrGly-----AsnAsnLeuAsp 496
Db 2374 ATAATTAATGTAATAAAGTGAACCACTCGGTACTCAATTAACCTTAATATATGCGCAT 2433
Qy 497 ValLeuThrTyrThrAsnProSerTyrProAsnLeuAspHisGlnArgSerValLeuPhe 516
Db 2434 ACATTAATTGATCCGCGGGTAACCTGTATATAATTAGCTAAAGGCGCAACGTTAGATT 2493
Qy 517 IleAsnLysLysTyrPheLeuValIleAspArg----- 527
Db 2494 AGTTATCAAAAACAATACTCTGTGATGATCAGCAAAATTCACAAACACAGACAATTTGTT 2553
Qy 528 -----AlaIleGlyGluAlaThrGlyAsnLeuGlyValHisTrpGlnLeu 542
Db 2554 GCAACACCGTTATCTCTCAGGTAAAGCCCTAAAATGCAAAATTAATATATGCAATA 2613
Qy 543 LysGluAspSerAsnProValPheAspLysThrLysAsnArgValTyrThrTyrArg 562
Db 2614 GCCATAGAAGCA-----CAAGATAATAAAGCGCTGAATACACCGTATTGCGAG 2661
Qy 563 AspGlyAsnAsnLeuMetIleGlnSerLeuAsnAlaAspArgThrSerLeuAsnGlu 582
Db 2662 CATATAAT-----CACTTCATGCTAGTAATAAGATAATAAATCACGCAAGAA 2706
Qy 583 GluGlyLysValSerTyrValTyrAsnLysGluLeuLys----- 595
Db 2707 GAGGGA-----TATGCTTTTTTAATGCCACCGCAAGTCAATTCATCTCAAGCTTTA 2757
Qy 596 -----ArgProAlaPheValPheGluLysProLysLysAsnAlaGlyThr 610
Db 2758 TTATTATCAAGTATGATCCCACTATGTTATGTTATGTTATGTTATGTTATGTTATGTTAT 2808
Qy 611 GlnAsnPheValSerIleValTyrPro-----TyrAspGlyGlnLysAlaPro 626
Db 2809 CAATTAACGCTAAGTATTGTTAATCTGATTTAATTAATTAATTAATTAATTAATTAATTAAT 2868

Qy 627 GluIleSerIleArgGluAsnLysGlyAsnAspPheGluLysGly----- 641
Db 2869 CAATTT-----GATAATTAAGGTAAACAGGTGAGTGAAGTGTATTATTCTCGCA 2919
Qy 642 -----LysLeuAsnLeuThrLeuThrIleAsnGly 651
Db 2920 TGGCTTACAGCGCATCTCAACCAATAAGTAGTAGTACTTACTGTAAAAGGG 2970

RESULT 12
US-08-956-171E-268/c
; Sequence 268, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 268:
US-08-956-171E-268

Alignment Scores:
Pred. No.: 0.0138 Length: 4702
Score: 116.00 Matches: 138
Percent Similarity: 33.20% Conservative: 103
Best Local Similarity: 19.01% Mismatches: 301
Query Match: 3.32% Indels: 185
DB: 4 Gaps: 27

US-09-802-285A-2 (1-659) x US-08-956-171E-268 (1-4702)

Qy 4 LysIlePheLysArgIleValPheAlaValIleAlaLeuSerSerGlyAsnIleu 23
Db 3000 AAAATATTCCAGGAGTTTCTAGTTATGCAATGATTAAGATGAGTCCAGAGGAAATCAGA 2941
Qy 24 AlaGlnSerSerIleThrArgLysAspPheAspHisIleAsnLeuGluTyrSerGly 43

Db 2940 GCAAAATCGCAATCTTACGGCAAGGTTCA---GACCAAAATCCGTCAAATTTTATCTCAT 2884
Qy 44 LeuGluLysValAsnLysAlaValAlaAlaGlyAsnTyrAspAlaAlaLysAlaLeu 63
Db 2883 TTAACMCGTGCACAGGTGAATTCGCGG---AACTGGGAAGTCAAGCT----- 2836
Qy 64 LeuAlaTyrArgGluLysSerLysAlaArgGluProAspPheSerAsnAlaGluLys 83
Db 2835 TTCAGCCGTTTCGAGAGCAATTCACAACACTTAGTCCT-----AAAGTAGAAAAA 2785
Qy 84 ProAlaAspIleArgGlnProIleAspLysValThrArgGluMetAlaAspLysAlaLeu 103
Db 2784 TTTGCACAATATTAGAGAAATTAACAACAATTAAGATAGCAGCTGCGCTGCTTCAA 2725
Qy 104 ValHisGlnPheGlnProHisLysGlyTyrGlyTyrPheAspTyrGlyLysAspIleAsn 123
Db 2724 GAACAAGACCAACACTTCTTAATAATTTCCGT----- 2692
Qy 124 TrpGlnMetTrpProValLysAspAsnGluValArgTrpGlnLeuHisArgValLysTrp 143
Db 2691 -----TTGCAATAAGCATTTCTGAAATTCGCAAAAGTCACAT-TTTCTAATG 2648
Qy 144 TrpGlnAlaMetAlaLeuValTyrHisAlaThrGlyAspGlu-----LysTyrAlaArg 161
Db 2647 TGGCTTTCCTATCATCTTTTAAAGAAACAACACTGAAAGGAATAAGCATGAAAGAAA 2588
Qy 162 GluTrpValTyr----- 165
Db 2587 AATTGGATTATGCAATTAATGTCACCTTTAATTATTATAATTGCCATAGTTAGTATGATA 2528
Qy 166 -----GlnTyrSerAspTrpAlaArgLysAsnProLeuGlyLeuSerGln 180
Db 2527 TTTTGTTCACCAAAATATGAGATCAATCAGAAAAGGATCCCAAAGTGTAAGTAA 2468
Qy 181 AspAsnAspLysPheValTyrArgProLeuGluValSerAspArgValGlnSerLeuPro 200
Db 2467 AAAATAATATA-----ATACATATCGCAATTTGTTAACAGAGATCAACCA 2423
Qy 201 ProThrPheSerLeuPheValAsnSerProAlaPheThrProAlaPheLeuMetGluPhe 220
Db 2422 ACGCATATAAC-----GGTAAAAAGTTGAGCTGGGTCAAGCATTTATTAAAGGTTA 2369
Qy 221 LeuAsnSerTyrHisGlnAlaAspTyrLeuSerThrHisTyrAlaGlu----- 237
Db 2368 GCAAAATGAGAAAACCTATAAATTTGAAAACAGTAAACAAGAAACGTTGCTGAGTCTGTTG 2309
Qy 238 ---GlnGlyAsnHisArgLeuPheGluAlaGlnArgAsnLeuPheAlaGlyValSerPhe 256
Db 2308 AAAAATGTTGATACCAAGTCATGATTGTTATCCAGAAAACCTTTTCAAAATGGCAATG 2249
Qy 257 ProGluPheLysAspSerProArg-----TrpArgGlnThrGlyIleSer--- 271
Db 2248 CAATTAGACGCTAAACACCACTCGAAAATATCGCTACAGTATAAAAACAGCTGTAGACAA 2189
Qy 272 -----ValLeuAsnThrGluIleLysLysGlnValTyrAlaAspGlyMetGln 287
Db 2188 AAAGAAGAAGTAGCTAAACACACAGAAAAGTTGTAAGTAATGTACTTAACGACTTTAAC 2129
Qy 288 PheGluLeuSerProIleTyrHisValAlaAlaIleAsp----- 300
Db 2128 AAAAATCTAGTCGAATTTATTACAGCATCATTTGATAATTTACATAATGCCAAAAA 2069
Qy 301 -----IlePheLeuLysAlaTyrGly-----SerAlaLysArg 311
Db 2068 AATGTTGGCGCTATTACGCGGTGAACATGTTGTAATAGTAAATTTCTCGAATTACTTA 2009
Qy 312 ValAsnLeuGluLysGluPheProGlnSerTyrValGlnThrValGluAsnMetIleMet 331
Db 2008 TTAATTCGAATTAACGACTTCCCGGAATTTATTACAGATACGCTTGTAATTCATTTCT 1949
Qy 332 AlaLeuIleSerIleSerLeuProAspTyrAsnThrProMetPheGlyAspSerTrpIle 351

Db 1948 GCAACAAAGACATTACA----- 1931
Qy 352 ThrAspLysAsnPheArgMetAlaGlnPheAlaSerTrpAlaArgValPheProAlaAsn 371
Db 1931 ----- 1931
Qy 372 GlnAlaIleLysTyrPheAlaThrAspGlyLysGlnGlyLysAlaProAsnPheLeuSer 391
Db 1930 -----AAATGGTTCCTCAACA-----TACAAAT 1910
Qy 392 LysAlaLeuSerAsnAlaGlyPheTyrThrPheArgSerGlyTrpAspLysAsnAlaThr 411
Db 1909 AAATCATTTATGAGTGGCAATTCAGATACGTTTCAGAGTGAACACAGATATATATGTTTCG 1850
Qy 412 ValMetValLysAlaSerProProGlyGluPheHisAlaGlnProAspAsnGlyThr 431
Db 1849 ACTTTAATTGAAMAA-----CAAAATTCATTAA 1823
Qy 432 PheGluLeuPheIleLysGlyArgAsnPheThrProAspAlaGlyValPheValTyrSer 451
Db 1822 TTTGAC-----GAGCACAATACAGCATGAGTAAATGTTTACAGATTATATAA 1775
Qy 452 GlyAspGluAlaIleMetLysLeuArgAsnTrpTyrArgGlnThrArgIleHisSerThr 471
Db 1774 TCGCAAAAAGATAGCTGGAACTTGATACTAT-----ATCAATGCATTA 1730
Qy 472 LeuThrLeuAspAsnGln-----AsnMetValIleThrLysAlaArgGln 486
Db 1729 AAACAGATGGACAGCAAAATGATCAACAATCAAGTATGATCAAGATACAGGTAAGAAGAA 1670
Qy 487 AsnLysTyrGluThrGlyAsnAsnLeuAspValLeu-----ThrTyrThr 501
Db 1669 TATAAACAACCTGTTAAAGAAAACCTTAGATAAAATAGAGAAATCATTCATCAACACAGAG 1610
Qy 502 AsnPro---SerTyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsnLysLys 520
Db 1609 TCACCATTTTCAAAAGGTATGATTGAAGANTATCGTAAGCAATTAACAGATCACTGCAC 1550
Qy 521 TyrPheLeuValIleAspArgAlaIleGlyGluAlaThrGlyAsnLeu----- 536
Db 1549 GATGAGCTTGCAAAATAACAAAGACTTACAAGATGCGCTAAATAGCATTAATAATGAACAAT 1490
Qy 537 -----GlyValHisTrpGlnLeuLysGluAspSerAsnProValPheAsp 551
Db 1489 GCTCAATTCGCTGAAAACCTTAGAGAAAACACTTCATGATGATATGTCGAAGAACTTGAT 1430
Qy 552 LysThrLysAsnArgValTyrThrTyrArgAspGlyAsnAsnLeuMetIleGlnSer 571
Db 1429 ACAGATACAACATTTATCTAT-----AACATGCTCAACACAGAC 1391
Qy 572 LeuAsnAlaAspArgThrSerLeuAsnGluGluGlyLysValSerTyrValTyrAsn 591
Db 1390 TTTTATAGCT-----GCAGGTTTAAATGAGGTGAAGCTAATAATACGAACAATTTGTC 1337
Qy 592 LysGluLeuLysArgProAlaPheValPheGluLysProLysLysAsnAlaGlyThrGln 611
Db 1336 AAAGAGCAAAACGTTATAAAAATGAATATATTTGAAAAAACCCGTTAGCAGAACACATT 1277
Qy 612 AsnPheValSerIleValTyrProTyrAspGlyGlnLysAlaProGluIleSerIleArg 631
Db 1276 AATTTTAACAGAT-----TACGATAACCAAGTTGCGCAAGACACAGATAGTTTG 1229
Qy 632 GluAsnLysGlyAsnAspPheGluLysGlyLysLeuAsnLeuThrLeuThrIleAsnGly 651
Db 1228 ATTTATGATGTTGTCAAAGTGCACGCTACTGAA-----ACGATTAAAAAGTAATGAT 1178
Qy 652 LysGlnGlnLeuValLeu 657
Db 1177 ATTTATCAATTAACGTGT 1160

RESULT 13

US-09-220-132-20

; Sequence 20, Application US/09220132

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; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 13993
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-220-132-20

Alignment Scores:
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Score: 116.00 Matches: 104
Percent Similarity: 30.99% Conservative: 94
Best Local Similarity: 16.28% Mismatches: 197
Query Match: 3.32% Indels: 244
DB: 4 Gaps: 26

US-09-802-285A-2 (1-659) x US-09-220-132-20 (1-13993)

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QY 231 -----LeuSerThrHisTyrAlaGluGlnGlyAsn 240
DB 9262 CAAAGTAAGTCTAGTTCAATCAGTATAAGTACAAACCAAAATTTCTCTGCTGGAACAAC 9321
QY 241 HisArgLeuPheGluAla-----GlnArgAsnLeu----- 250
DB 9322 GAGAACATTATGAGGCCCATGTAGGAATAAATGGAGAACAAATCTGGATTTCTTAAAC 9381
QY 251 -----PheAlaGlyValSerPheProGluPhe 259
DB 9382 ATTCCCTTAAACATCTCGAAATCGCTACCTTACCAATAATACCAATCTCTCCACTG 9441
QY 260 LysAspSerProArgTrpArgGlnThrGly----- 269
DB 9442 AAAGATTTCTCTATATGGGAAAAAACAGGCTTGAAGGAATTTCTTGAACACGACAAAGCAA 9501
QY 269 ----- 269
DB 9502 TCATTTGATTTAAGTGAAGCTCAGTATAAGAAACAAACACAGGCATTCATCACA 9561
QY 270 -----IleSerValLeuAsnThrGluIleLysGlnValTyrAlaAspGlyMetGln 287
DB 9562 AATCCTTTGGCTGTGCTTGTGAGTTATCAGTCAGAGCATCAATCTTTGACAGGCAT 9621
QY 288 PheGluLeuSerProIleTyrHisValAlaAlaIleAspIlePheLeuLysAlaTyrGly 307
DB 9622 TTTGAAAAAACC-----AGAAACAATGCATTTAGATTTTGTTCACCAATCTCTATAAT 9672
QY 308 SerAlaLys-----ArgValAsnLeuGluLys-----GluPheProGln 320
DB 9673 GAACAAAAAATTAAAGTTTGTAGTACAAAGCTGAAAAATCTCAGCAGAGCTCCCGAGG 9732
QY 321 SerTyrValGlnThrValGluAsnMetIleMetAlaLeuIleSerIleSerLeuProAsp 340
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QY 341 TyrAsnThrProMetPheGlyAspSerTyrIleThrAspLysAsnPheArgMetAlaGln 360
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DB 9787 TTCACCATAGAGATGCGGCAATCGGTATGTCTCCAAAAGCAGTCAGCATGCGCTAGT 9846
QY 377 PheAlaThrAspGlyLysGlnGlyLysAlaProAsnPhe----- 389
DB 9847 TTTCTCCATCATAGGTCTTGACGTCGCTGCTTCATACACATTAATCCTGCCATCAATTA 9906
QY 389 ----- 389
DB 9907 GAGTCGCCAGTCTTCATGTCCTAGAAATCTCAAGCTTTCTCTCCAGATTTTCAAGAA 9966
QY 390 -----LeuSerLysAlaLeuSerAsnAlaGlyPhe-----TyrThr 401
DB 9967 TTGTGTACCATAAAGCCATATTTTATTCCTGCCATATTAATACCTATGATTTCTCC 10026
QY 402 PheArgSerGlyTrpAspLysAsnAlaThrValMetValLeuLysAlaSerProGly 421
DB 10027 TTTAAATCAAGT-----GTATCACATGAATACCAATGCT 10062
QY 422 GluPheHisAlaGlnProAspAsnGlyThrPheGluLeuPheIleLysGlyArgAsnPhe 441
DB 10063 GAACTTTTAAACAGTCAGAT-----ATTGTTGCTCATCTCTCTTCTTCATCTTCATCT 10116
QY 442 ThrProAspAlaGlyValPheValTyrSerGlyAspGluAlaIle----- 456
DB 10117 GTCATTGATGCACTGCGACTACAAATTAGAGGGGCCACCAAGATTCAGAAAGAAAGGGGA 10176
QY 457 -----MetLysLeuArgAsnTrpTyrArgGlnThrArgGlnThrArgIleHisSer 470
DB 10177 TTGAAGTTAGCCACAGCTCTGCTCTGAGCAAATAATTTGAGGGTACTCATACAGT 10236
QY 471 ThrLeuThrLeuAspAsnGlnAsnMetValIleThrLysAlaArgGlnAsnLysTrpGlu 490
DB 10237 ACTGTGAGCTTAACACGAAATAATGGAAGTGTGAGTGGCAAAACCAAAACCGGAA 10296
QY 491 -----ThrGlyAsnAsnLeuAspValLeu 498
DB 10297 ATTCCAATTTTGAAGATGAATTTCAAGCAAGAACTTAATGGAATATCAAGTCAAAACCT 10356
QY 499 ThrTyrThrAsnProSerTyrProAsnLeuAspHisGlnArgSerValLeuPheIleAsn 518
DB 10357 ACTGTCTCTCTCCATGGAATTTAAGTATGATTTCAATTTCTCAATGCTGCTACTACC 10416
QY 519 LysLys-----TyrPheLeuVal 524
DB 10417 GCTAAAGGAGCAGCTTGACCAAGCTTAGCTTGGAAAGCCTCACCTCTTACTTTCCATT 10476
QY 525 IleAspArgAlaIleGlyGluAlaThrGlyAsnLeu----- 536
DB 10477 GAGTCATCTACCAAGAGATGTCAAGGTTTCGGTCTTCTCGGGAATATTACAGNACT 10536
QY 536 ----- 536
DB 10537 ATTGCTAGTGAGGCCAACACTTACTTGAATTTCAAGAGACACACGCTTTCAGTGAAGCTG 10596
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DB 10597 CAGGGCAGCTTCCAAATGTATGATATCTGGAACCTTGAAGTAAAGAAAAATTTGCTGGA 10656
QY 551 AspLysThrLysAsnArgValTyrThrTyrArgAspGly-----AsnAsnLeuMet 568
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QY 569 IleGlnSerLeu-----AsnAlaAspArgThrSer-----LeuAsnGluGlu 582
DB 10717 CTAGAGGGCTCTTTTTCACCAACGGAACATACAAAGCAAAACCCCTCTCTCTCT 10776
QY 583 GluGlyLysValSerTyrValTyrAsnLysGluLeuLysArgProAlaPheValPheGlu 602
DB 10777 CAGTGGCAATGTACGCTCTTGTTCAGGTCATGCAAGTCAGCCAGCTTCTTCCATGAT 10836
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2004, 17:26:51 ; Search time 49 Seconds
(without alignments)

4211.605 Million cell updates/sec

Title: US-09-802-285A-2

Perfect score: 3494

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	243	7.0	896	12	US-10-282-122A-45584 Sequence 45584, A
2	130.5	3.7	681	12	US-10-282-122A-71561 Sequence 71561, A
3	128	3.7	25	9	US-09-802-285-3 Sequence 3, Appli
4	128	3.7	25	14	US-10-231-337-3 Sequence 3, Appli
5	126.5	3.6	696	12	US-10-282-122A-70746 Sequence 70746, A
6	123	3.5	532	15	US-10-369-493-22074 Sequence 22074, A
7	120	3.4	677	15	US-10-369-493-23212 Sequence 23212, A
8	118.5	3.4	579	15	US-10-369-493-2315 Sequence 2315, Ap
9	118.5	3.4	579	15	US-10-369-493-2321 Sequence 2321, Ap
10	117.5	3.4	1484	12	US-10-335-977-8966 Sequence 8966, Ap
11	117.5	3.4	2902	12	US-10-282-122A-59042 Sequence 59042, A
12	117	3.3	1163	15	US-10-452-024-107 Sequence 107, App
13	117	3.3	1250	10	US-09-769-736-10 Sequence 10, Appl
14	116	3.3	919	12	US-10-282-122A-70737 Sequence 70737, A
15	116	3.3	4563	10	US-09-802-640-32 Sequence 32, Appl

16	116	3.3	4563	12	US-10-403-902A-32 Sequence 32, Appl
17	115.5	3.3	987	12	US-10-282-122A-48445 Sequence 48445, A
18	115.5	3.3	1314	15	US-10-369-493-1532 Sequence 1532, Ap
19	115.5	3.3	1331	9	US-09-801-368-370 Sequence 370, App
20	114.5	3.3	645	14	US-10-130-973A-8 Sequence 8, Appli
21	114.5	3.3	1279	10	US-09-882-227-388 Sequence 388, App
22	114	3.3	871	15	US-10-369-493-13471 Sequence 13471, A
23	114	3.3	899	15	US-10-369-493-5864 Sequence 5864, Ap
24	114	3.3	2234	12	US-10-282-122A-46565 Sequence 46565, A
25	113.5	3.2	1398	12	US-09-841-553-8 Sequence 8, Appli
26	113.5	3.2	1398	13	US-10-090-624-6 Sequence 6, Appli
27	113	3.2	2179	14	US-10-224-999A-3481 Sequence 3481, Ap
28	111.5	3.2	846	15	US-10-320-797-3302 Sequence 3302, Ap
29	111.5	3.2	962	12	US-10-282-122A-77946 Sequence 77946, A
30	111	3.2	723	15	US-10-369-493-10942 Sequence 10942, A
31	110.5	3.2	563	9	US-09-815-242-5665 Sequence 5665, Ap
32	110.5	3.2	578	9	US-09-815-242-12206 Sequence 12206, A
33	110	3.1	4563	9	US-09-870-759-128 Sequence 128, App
34	110	3.1	4563	10	US-09-751-708A-128 Sequence 128, App
35	109.5	3.1	966	15	US-10-099-322-72 Sequence 72, Appl
36	109.5	3.1	966	15	US-10-044-564-72 Sequence 72, Appl
37	109.5	3.1	1465	12	US-10-282-122A-47271 Sequence 47271, A
38	109	3.1	634	12	US-10-282-122A-52070 Sequence 52070, A
39	107.5	3.1	1336	10	US-09-934-455-22 Sequence 22, Appl
40	107.5	3.1	1336	12	US-10-412-699B-654 Sequence 654, App
41	107.5	3.1	1336	12	US-10-225-066A-576 Sequence 576, App
42	107.5	3.1	1336	14	US-10-278-173-128 Sequence 128, App
43	107.5	3.1	1336	15	US-10-225-067-92 Sequence 92, Appl
44	107.5	3.1	1336	15	US-10-374-780A-204 Sequence 204, App
45	107	3.1	477	12	US-10-335-977-9400 Sequence 9400, Ap

ALIGNMENTS

RESULT 1

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US-10-282-122A-45584
; Sequence 45584, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
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213	Qy	TPAFLMFB-----LNSVHQQADLYLTHYAEQG--NHRLF--BAORNLPAFAGVSPPEF	259
238	Db	QKKWVMQVSVNGAVGSGSGMQYFVGCDPDGTHFKNENPNKVLWTDYGRDFYAAVSWSDI	297
260	Qy	--KOSPR-----WRQTGISVLNTEIKQVYADGQMOFELSPYHVA	298
298	Db	PSTDSSRLWLGWMSNWQYANDVPTSPWRSAA--TSIPRELKKAFTGEGRVVQTPVKELET	355
299	Qy	I-----DIFLKAYGSAKRVNLE--KEPPQS-----VYQTVENMIM--	331
356	Db	IRGTSKKWKNLTI SPASHNVLAGQSGDAYEINAEFKVSGFSAAEQFKVKTGCGOFTKVG	415
332	Qy	-----ALISLDPVNTPMFGDSWITDXN-----FRMAQFASMARVPFPAQAIKYFATDGGKQ	383
416	Db	YDRRNAKLFVDRSESGNDTFPAFTGKETAPLKPVGNGVKLRIIFVDRSSVVFVNGDGGKQ	475
384	Qy	GKA-----PNFLSKAL-----SNAG-----FYFRSGWDKNATVWLK	416
476	Db	VITDIILPDRSKGLGYAANGGVKVSILTHPLKKVGTTPFMSNMTCW-----TTV-----	528
417	Qy	ASPGEEFHAQPDNGTFELFIKGRNFTPDAGVFVYS-----GDEA	455
529	Db	-----NGTWADTIEGKQGRSGDGSFILSSAGSDTFYESDITIKDNGRGAGA	576
456	Qy	IMKLKNWYQTRIHSITLLDNONMVIITKARQNKWETGNLNLVLVTNPSYPLNDHQRSVL	515
577	Db	LM-----FRSKDAKNGLYANVDKADHLVKFPKFENGGAASVIAEYKTP-----I	620
516	Qy	FINKYFL-----VIDRAIGBA-----TGNLGVH--WQLKEDSNPVF	550
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RESULT 8

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? Sequence 2315, Application US/10369493
? Publication No. US20030233675A1
? GENERAL INFORMATION:
? APPLICANT: Cao, Yongwei
? APPLICANT: Hinkle, Gregory J.
? APPLICANT: Slater, Steven C.
? APPLICANT: Goldman, Barry S.
? APPLICANT: Chen, Xianfeng
? TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
? TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
? FILE REFERENCE: 38-10(52052)B
? CURRENT APPLICATION NUMBER: US/10/369,493
? CURRENT FILING DATE: 2003-02-28
? PRIOR APPLICATION NUMBER: US 60/360,039
? PRIOR FILING DATE: 2002-02-21
? NUMBER OF SEQ ID NOS: 47374
? SEQ ID NO 2315
? LENGTH: 579
? TYPE: PRT
? ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2315

```

Query:

QY	171	AKKPLUGSQNDKRFVWKLPLEVSQKUSLPTFLSVNSPAPTAPFLMEFLNSYHQADY	233
Db	125	SKTNP-----KRDWYFWKPYRNEKGERLPP-----NNMRSYFDT	159
QY	231	LSTHVAEQNHRLFEAQRLNFAGVSYSPFEK--DSPRWOTGISVLNTEIKQVYADGMOPE	289
Db	160	SAWEWDATQ-----EYIHLWS--VGQDPLNWETPKVREAVHDIURFWLDRGV--DG--FR	210
QY	290	LSPIYHVAADIFLKA-----YGSAKRVNLEKPEPQSQVQTVENNIMALI	334
Db	211	LDALNMISKQOREFDADPTTDDRYEQYQAYQYANGPRIH-----EYUNGIGNI-----	258

QY 335 SISLPDNTPMFGD-SWITDKN-----FRMAQFASWARVFPANQAIKYPATD 380
Db 259 ---LTHDAPSVGEMPYVLTNELLHVVGADRELTWIFQDFVDLDPNQH-KIEGS 314
QY 381 GKGQKAPNLSK----ALSNAGF-YTPRSQMDKNATV-MVLKASPPGEPHAQPDNGTFEL 434
Db 315 WELSDLKSLKKWQSALLSGGWNASFIENHDQTRTVSRVLSDSPKYRAYSSKLMALFII 374
QY 435 FIGRNFPTDAGVGVVSGDAIMKLRNWWYQTRIHSTLTLDNQMVITKARQNKWETGNN 494
Db 375 FQSG---TP----FVFGQE--LALANIPRDWPIDEYLDVETQNF-----WK----- 412
QY 495 LDVLTNPSYPNLDHORSVLEFNKYFLVIDRAIGEATCNLGVHWQKEDSNPVFDKTK 554
Db 413 --LFMSGNPQOEI--EKTMDIVNKR-----ARDNGRTPMHW-----DSSPENGFTK 455
QY 555 -----NRVYTYRDGNLMIQSLNADRTSLNBEEGKVS-----VYNKELK 595
Db 456 AGVKPMWRVTNDYKEWN-----AANQVNDPESPYTFWSKALELRKELK 498

RESULT 10

US-10-335-977-8966
; Sequence 8966, Application US/10335977
; Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 8966:
SEQUENCE CHARACTERISTICS:
LENGTH: 1484 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori

FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1484
SEQUENCE DESCRIPTION: SEQ ID NO: 8966:
US-10-335-977-8966

Query Match 3.4%; Score 117.5; DB 12; Length 1484;
Best Local Similarity 18.1%; Pred. No. 0.84;

Matches 120; Conservative 100; Mismatches 257; Indels 187; Gaps 29;
QY 86 DIRQPIDKVTREMA--DKALVHQFQPHKGYGYDYDKD-INWQWPVKDNEVRLHRVK 142
Db 600 DIVKPSDALKNDVAALGKQMIGF-----LQODTLNSLESLLQNOQIKSVLDKVL 649
QY 143 WQAMALVY-HATGD--EKYAREWVYQYSDWARKNPLGLSQDNDKFWVRPLEVSDRVQSL 199
Db 650 AAKGLASIEVOGLGDLIPNLGKKGIFA-----PYGLSQ-----VWQGDSEFNAQ-- 695
QY 200 PPTFSLFVNSPAFTPA--FLMEF-----LNSYHQQADYLSHY 235
Db 696 ---NVFQNSTESNANGGTLSTFNAGSLIFAGNNHIAFTNHSGLTNLLSNQVSNINVTM 751
QY 236 --AEQG-----NHLFEAQNLIFAGVSPFEFKDSRWRQTG----- 269
Db 752 LNASGLKINATNNNSVSGNLFINASCVOQSDPTTASATNCTTAQNNASSNASNNA 811
QY 270 -ISVLNTEIKKQVYADGMQFELSPIYHVAIDIFLKAYGSA----- 309
Db 812 PIALNNDESLLVTANGFNS-GNIYANGVVD-FSKIGSANVKNLYLYNNAQFQANNLT 869
QY 310 -----XRVNLEKEFFPOSYVQTV--NMIMAL-ISISLPDYNTPMFGDSW 350
Db 870 ISNQAVLEKNASFVTNNLNIQGAFFNNNATOKIEVLQNLVIASNASLSTGIYGLEVG-- 926
QY 351 ITDKNFERMAQFASWARVFPANQAIKYFATDGKQKAPNFLSKALSNAAGFYTFERSGWDKNA 410
Db 927 -ALNNGAIHFNLENSQTPVNPLIQVGIINLNTQTTPMNVSVANGGTVT----- 976
QY 411 TVMVLKASPPGEFHAQPDN--GTFELF-----IKGRNFTPDAGVGVSGDEAIMKLRNWR 464
Db 977 ---LLKSSRYIDYNINPNSLSQYLKLYTLNINGNHIEEKNGVLYLQORVLLQDKGLL 1033
QY 465 QTRIHSTLTLDNQMVITKARQNKWETGNLVDVLYTNPSYPNLDHORSVLFNKKYFLV 524
Db 1034 SVALPNSNNASQNNILSLSVLHNQIKMSYGNKVMDEPTPTL-----QDYIVGIGQGSALN 1088
QY 525 IDRAIGEATCNLGVHW-----QLKEDSNPVFDKTKNRVYTYRDGNLMIQSLNADRTSLN 580
Db 1089 QIEAVG---GNNALKWLSTLMMETKENPLF-----APIYLEHSLN 1126
QY 581 EEEGKVSYYVYNKELKRPAPFVEKPK-KNAGTONFVSIVYPYDQKAPFIS---IRENKN 636
Db 1127 EILG-----VTKDLQNTASLISNPNFNATSLLEMASYQTQTSRLTKLSDFRAREGESN 1181
QY 637 DFEK 640
Db 1182 FSR 1185

RESULT 11

US-10-282-122A-59042
; Sequence 59042, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078


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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59042
; LENGTH: 2902
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-282-122A-59042

Query Match          3.4%; Score 117.5; DB 12; Length 2902;
Best Local Similarity 18.1%; Pred. No. 2.4;
Matches 120; Conservative 100; Mismatches 257; Indels 187; Gaps 29;

Qy 86 DIRQPIDKVTREMA--DKALVHQFQPHKGYGYFDYKGD-INMQMVPKDNVNRWOLHRVK 142
Db 2018 DIVKPSDALKNDVAALGKQMGIEF-----LGQDTLSLESLLQNOQIKSVLDKVL 2067

Qy 143 WQAMALVY-HATGP--EKYAREWVYQSDWARKNPLGLSQDNDFKVRPLEVSRVQSL 199
Db 2068 AAKGIGSYIEQGLGDLIPNLGKKGIFA-----PYGLSQ-----VMQKGDFFSNAQG-- 2113

Qy 200 PPTFSLFVNSPAFTPA--FLMEF-----LNSVHQQADYLSHY 235
Db 2114 ----NVFQNSTFSNANGGTLTSFNAGNSLIPAGNHHIAFTNHSGLTLLNSQVSNINVTM 2169

Qy 236 --AEGG-----NHLFEAQRNLPAGVSPPEPKDSPRWRTG----- 269
Db 2170 LNASGLKINATNNVSVSQGLFNASCVOQSDPTTASATNPCTTAQNNASSNASNNA 2229

Qy 270 -ISVLNTEIKQVYADGMQFELSPIYHVAADIFLKAYGSA----- 309
Db 2230 PIALNNDESLVVTANGFNFS--GNLYANGVVD-FSKIKGSANVKNLYLYNNAQFOANNIT 2287

Qy 310 -----KRYNLEKEFPQSYVQTVVE---NMIMAL-ISISLPDVTNTPMFGDSW 350
Db 2288 ISNQAVLEKNASFVTTNLIQGAFFNNAQTQIEVLQNLVIASNASLSGTGIYGVGG--- 2344

Qy 351 ITDKNFRMAQASWARVPANQAQIKVATDQKQKAPNPLSKALSNAGFYTPRSQWDKNA 410
Db 2345 -ALANNLGAHFLENLSQTPVNPVLIQVGGIINLTNTTQTPFMVSVANGGTYT----- 2394

Qy 411 TVMVLKASPPGFEHAQPN--GTFELF---IKGNFTPDAGVFVYSGDEALMKLRNWR 464
Db 2395 ---LUKSGRYDININPNSLQYKLYTLININGNHIIEKNGVLTYLQORVLLQDKGLL 2451

Qy 465 QTRIHSTITLDQNQVITKARQNKWETGNNLDVLTYPNPSYNPLDHRQSVLPINKKYFLV 524
Db 2452 SVALPNSNKNASQNNILSLSLVHNLQIKMSYGNKVMDFTPETL-----QDYIVIGIQCSALN 2506

Qy 525 IDRALGEATGNLGVW----OLKEDSNPVFDTKNRVYTYTDRDGNMLQSLNADRTSLN 580
Db 2507 QTEAVG---GNNAIKWLSTLMMETKENPLF-----APIYLENHSIN 2544

Qy 581 BEEGKVSYYNKEKLPAPVFEKPK-KNAGTQNFVSIVVYPYDQKAPETIS---IREKN 636
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Db 2545 EILG-----VTKDLQNTASLISNPNFRNATSLLEMASYTOQTSLTKLSDFRAREGSN 2599
Qy 637 DPEK 640
Db 2600 FSR 2603

RESULT 12
US-10-452-024-107
; Sequence 107, Application US/10452024
; Publication No. US20040013687A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Lance
; APPLICANT: Park, Jung-Beak
; APPLICANT: Maksymowich, Andrew
; TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
; FILE REFERENCE: 9855-96U1
; CURRENT APPLICATION NUMBER: US/10/452,024
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/384,949
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-452-024-107

Query Match          3.3%; Score 117; DB 15; Length 1163;
Best Local Similarity 17.1%; Pred. No. 0.64;
Matches 141; Conservative 129; Mismatches 280; Indels 274; Gaps 38;

Qy 17 LSSGNILAQSSSITRKDF-----DHNLEYSGLKVKVKAAGNYDDAAKALIA 65
Db 380 LKMSNVYGDGLGTWNNFYAVYKIPYNGIDFVHNSYLNVN--VEEINNIPPINDADIY 438

Qy 66 YYREKSKAREPDFS-----NAEKPADIROPIDKVR-----EMADKALV 104
Db 439 PYRKNSDPFPYVINITETKEINTTTPLSVNYLQAQVTSNDINLSDFSIVSLKDRSLV 498

Qy 105 HQFQHKGYGYFD--YKGDIN-----WQMPVKDNVNRWOLHRVW 144
Db 499 YSFLDNT-IDYLDSTIKYDEPINTDKKYYLWLKBIFRNYSFDMTEIQEWNIPCGINKRVPM 557

Qy 145 QAMALVYHATGDEKYAREWVYQSDWARKNPLGLSQDNDFKVRPLEVSRVQSL----- 199
Db 558 LGKALNILNTGNS-----FIEFKTLGPISLINKKENIIMPKEIDEIPNSMLNSF 609

Qy 200 ----PPTFSLFVNSPAFTPAFLMEFINSYHQADYLSHY-----AEQ----- 238
Db 610 KDLSENLENIFFSKNSYFEKIYYDFLDQWWTQ--YYSQYFDLICMAKRSVLAEGLIKKI 667

Qy 239 -----GNHRLPE-----AQRN-----LFAGV 255
Db 668 IQKLSYILGNSISADNLVLMNLTITTLRDISNESQIAMNVDSFLNSAAICVFEGNI 727

Qy 256 PPEF-----KDSPRWRQTGISVLNTE-----IKQVYADGMQFELSPIYHVA 299
Db 728 YPKFISFMEQCINNINKNTRFIOKCTNITENEKQLINRNIFS-SLDFDFLINIEN---- 782

Qy 300 DIFLKAYGSAKRVNLEKEFPQSYVQTVNMMALISISLPDVTNTPMFGDSWITDKNFRMA 359
Db 783 ---LKSLSFSETALLIKEETSPYE-----LVLYAFQEPDNN--IGDA--SAKNTSIE 828

Qy 360 QFASWARYF-----PANQAIKYFATDGKQKAPNPLSKALSNAGFYTPRSQWDKN 409
Db 829 YSKDIDLVIINGDALYNGANQSLSF-----SNDFFENGLTNSFSYIF---WLRN 876

Qy 410 ATVMVLKASPPGFEHAQPNGTFFELFKRGNFTPDAGV-----YSGDEALMKLRNWR 465
Db 877 LGKDTIKSLIG--SKEDNCGWEIYFQ-----DTGLFVNMDSGNEXNIYLSDSNN 927
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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70737

Query Match      3.3%; Score 116; DB 12; Length 919;
Best Local Similarity 18.2%; Pred. No. 0.55;
Matches 124; Conservative 84; Mismatches 216; Indels 258; Gaps 31;

QY 56 YDDAAKALLAYREKSKAREPDFSNAEKPADIR-----QPIDKVTREMADK 101
DB 370 YDKANKAVTDLLEKADLLKLDFTHSYPHDWRTKKPVIFRATPQWFAFASINKVRQDILDA 429
QY 102 ALVHQFQPHKGVGYPDYGDINWQMPVKDNEVRWQLHRVQWQAMALVYHA-TGDEKYA 160
DB 430 IEDTNFK-----VDWGKTRIYNN--IRDRG-EWVISRQVRWGVPPLPVFAENGDIIMT 479
QY 161 REWVYQYSDWARKNPLGLSQNDKQVWRPLEVSDRVQSLPPTFSLFVNSPAPTFAFLMEF 220
DB 480 KETVNHVAD-----LFEKHGSNIWEKEAK---ELLPEGFS-HPGSPN----- 518
QY 221 LNSVHQADYLSTHYAEOGNHR-LPEAQRNLFAGVSFPE--FKDSPRWRTGIGSVLNTE 276
DB 519 -GEFTKETDIMDVWDSDSGSHRGVLETRPEL-----SFADLYFEGSDQYR---GWENSS 569
QY 277 IKQVYADGMOFELSPIYHVAAIDIFLKAYGSAKRVNLEKEPPQSYQVQTVQTVENMINALISI 336
DB 570 ITTAVATRGQ-----APYKFLLSHG----- 589
QY 337 SLPDYNTPMFGDSWITDKNFRMAQFASWARVFPANQAIKYFATDCKQKQKAPNFLSKALSN 396
DB 590 -----FVMDG-EGKK-----MKSLSLN 605
QY 397 AGFYTFRSGWKNATVMVLKASPPGFEHAQPDNGTFELFKGRNFTPDAGVFVYSGDEAI 456
DB 606 -----VIV-----PDQVVKQKGADIALWVSSTDYLSVRI-----SDEIL 641
QY 457 MKLRNWRQTR-----IHSTLTLDNQNNVITKARQNKWETGNNLDV 497
DB 642 KQTSVYRKIRNTRFELMGLNINDFNPETDSTAETNLLVEDRYLLNRLREFTASTINNYEN 701
QY 498 LTYTN-----PSYPN-----LDHORSVLFINKK-----YFLVIDRAIGBAT 533
DB 702 FDYLNIEVQNNFINVELSNFYLDYTGKDLILYIEKDSHKRSMQVVLQOILVD--MTKLL 759
QY 534 GNLGVH-----W-----OLKEDSNPVFDKTKN-----RVYTTYRDGNNLMIQSLN 573
DB 760 APILVHTAEVWMSHTPHVKEESVHLSDMPKVVDVDEELLEKWTENWLRDDVNRALEQAR 819
QY 574 ADRTSLNEEGKVSVYVYNKELKRPAPVFE-----KPKKNAGTQNFVSVIY 618
DB 820 NEKVIGKSLEAKVWIGSNESFNFAEFLOQFNDLQOLFIVSQVEVKDKVNDG-----VSY 873
QY 619 PYDGOKAPEISIRENKGNDFEK 640
DB 874 QYG-----DIHLKHAEGEKER 890

RESULT 15
US-09-802-640-32
; Sequence 32, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Klevn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
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; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-32

Query Match      3.3%; Score 116; DB 10; Length 4563;
Best Local Similarity 16.3%; Pred. No. 6.7; 197; Indels 244; Gaps 26;
Matches 104; Conservative 94; Mismatches 94;

QY 218 MEFINSY-----HQQADY-----LSTHYAEOGNHRLFEA-----QRNL----- 250
DB 3068 IDFLNNYALFALSPSAQQAQVSAFFNQYKYNQNFAGNENIMEAHVINGEANLDFLN 3127
QY 251 -----FAGVSFPFKDSPRWRTG----- 269
DB 3128 IPLTIPEMRLPYTIITTPPLKDFSLWEKTKFLKTKTKQSFDSLVSQAQYKKNKHSIT 3187
QY 270 --ISVIANTEIKQVYADGMOFELSPIYHVAAIDIFLKAYGSNAK---RVNLEK---RFPQ 320
DB 3188 NPLAVLCEFIQSQIKSFRHFEKN---RNNALDFVTKSYNETKIKFKYKAEKSHDELPR 3244
QY 321 SYVQTVENMINALISISLDPDYNTMFGDSWITDKNFRMAQF-----ASWARVFPANQAIKY 376
DB 3245 TF-----QIPGYTPVW-----NVEVSPFTIEMSAFGYVFPKAVSMES 3282
QY 377 FATDQKQKAPNF-----LSKALSNAGF-YT 401
DB 3283 FSIILGSDVRVPSYTIILPSELPLVHVPRLNKLSPHFKELCTISHIFIPAMGNITYDFS 3342
QY 402 FRSGWDKNATVMVLKASPPGFEHAQPDNGTFELFKGRNFTPDAGVFVYSGDEAI----- 456
DB 3343 FKSS-----VITLTNAELFNQSD--IVAHLSSSSSVIDALQYKLEGTRTRTKRG 3392
QY 457 -----MKLRNWRQTRIHSTLTLDNQNNVITKARQNKWE-----TGNLNDVL 498
DB 3393 LKLATALSLSNKFVEGSHNSVSLTTKNWEYSVAKTKAEIPLRMNFKQELNGNNGSKP 3452
QY 499 TYTNPSYPNLDHORSVLFINKK-----YFLVIDRAIGBATGNL----- 536
DB 3453 TVSSSMPEKYPDNSSMLYSTAKGAVDHHKLSLESLSYFESSTKGDYKSVLSREYSGT 3512
QY 537 -----GVH-----WQIKEDSNPVFDKTKNVRVYTYRDG--NNLM 568
DB 3513 TASEANTVINSKTRSSVKLGQTSKIDDIWNLEVENFAGEATLQRIYLSLWHSHTNHLQ 3572
QY 569 IQSL---NADRTS---LNEEEGKVSVYVYNKELKRPAPVFEKP-----KKNAGTQN----- 612
DB 3573 LEGLFTNGEHTSKATLELSPWQMSALVQVHASQPSSEFHPDPLDGLQEVALNANTKNQIR 3632
QY 613 FVSIVYPYDGOKAPEISIRENKGNDFEKGLNLTITING 651
DB 3633 WKNEVRIHSGSFQSQVEL-----SNDQEKAHLDIAGSLEG 3667

Search completed: July 27, 2004, 17:33:03
Job time : 53 secs
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